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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Tue Jul 25 22:23:21 2000; MasPar time 35.62 Seconds  $811.775\ \text{Million}$  cell updates/sec

Description: Perfect Score: >US-09-314-889-4 (1-417) from US09314889.pep 3198

Sequence: 1 MEQRPRGCAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP 417

Scoring table: РАМ 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl12
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 47.427; Variance 85.811; scale 0.553

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	рв	ID	Description	Pred. No.
<u>_</u>	3187	99.7	418	4.	000275	LYMPHOCYTE ASSOCIATED	0.00e+00
ν	2945	92.1	426	4	014865	DEATH RECEPTOR 3 BETA.	0.00e+00
ω	2483	77.6	380	4	000280	LYMPHOCYTE ASSOCIATED	0.00e+00
4	2451	76.6	372	4	000279	LYMPHOCYTE ASSOCIATED	0.00e+00
υı	1577	49.3	253	4	000276	LYMPHOCYTE ASSOCIATED	0.00e+00
6	1423	44.5	277	4	014866	SOLUBLE DEATH RECEPTOR	2.10e-289
7	1329	41.6	234	4	000278	LYMPHOCYTE ASSOCIATED	1.37e-267
8	467	14.6	126	4	000277	LYMPHOCYTE ASSOCIATED	4.18e-72
9	272	8.5	471	6	019131	TUMOR NECROSIS FACTOR-	3.50e-31
10	228	7.1	616	4	Q9Y6Q6	RECEPTOR ACTIVATOR OF	1.55e-22
11	218	6.8	327	6	097491	FAS PROTEIN.	1.27e-20
12	210	6.6	189	σ	097530	TUMOR NECROSIS FACTOR	4.16e-19
13	212	6.6	625	11	035305	RECEPTOR ACTIVATOR OF	1.74e-19
14	206	6.4	189	6	Q95185	TUMOUR NECROSIS FACTOR	2.35e-18
15	202	6.3	263	6	Q9xS60	FAS ANTIGEN SPLICED VA	1.31e-17
16	202	6.3	320	6	Q9xs29	C-TYPE FAS ANTIGEN.	1.31e-17
17	199	6.2	186	14	072735	A53R PROTEIN.	4.75e-17
18	198	6.2	186	14	Q9YP87	SOLUBLE TNF RECEPTOR C	7.28e-17
19	199	6.2	316	14	057092	TUMOR NECROSIS FACTOR	4.75e-17
20	194	6.1	186	14	Q9WJB4	TUMOUR NECROSIS FACTOR	3.99e-16

3 6.0 283 6 Q9XSZ8 3 6.0 283 4 Q9Z9Z8 3 6.0 314 4 Q14293 7 5.8 320 14 0577091 7 5.8 322 14 057712 8 5.6 348 14 057112 8 5.6 348 14 085407 9 5.6 349 14 085110 9 5.6 349 14 057111 9 5.6 349 14 057111 9 5.6 349 14 057111 9 5.6 349 14 057111 9 5.6 349 14 057111 9 5.6 349 14 057110 9 5.6 349 14 057110 9 5.6 349 14 057110 9 5.6 349 14 057110 9 5.6 349 14 057110 9 5.4 348 14 057108 1 5.4 348 14 057109 1 5.4 349 14 057291 1 5.4 349 14 057291 1 5.4 349 14 057291 1 5.4 349 14 057101 1 5.4 349 14 057101 1 5.4 349 14 057101 1 5.4 349 14 057101 1 5.4 349 14 057101 1 5.4 349 14 057101	Л	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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Biochem. Biophys. Res. Commun. 242:376-379(1998).
EMBL, AF026070; AAC39556.1; -.
HSSP; P19438; ITNR.
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01-JAN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
DEATH RECEPTOR 3 BETA.
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Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
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                                               PLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEA
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ilarity 94.18;
Conservative
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i; Hominidae; Homo.
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LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 8
(LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 5).
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PFAM;
           Homo sapiens (Human) Eukaryota; Metazoa;
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01-JUL-1997 (TIEMBLIEL 04, Last sequenc
01-NOV-1999 (TIEMBLIEL 12, Last annotat
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
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PFAM; PF00020; TNFR_C6; 2.
SEQUENCE 380 AA; 41192 MW;
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MEDLINE; 97272273.
SCREATON G.R., XU X.N., OE
MCMICHAEL A.J., BELL J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                         MEDLINE; 97272273.
SCREATON G.R., XU X.N., OL MCMICHAEL A.J., BELL J.I.;
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01-UUL-1997 (TREMBLrel. 04, Last Sequence update)
01-WU-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAY-1997) to the
                                                                                             PFAM; PF00020;
SEQUENCE 253
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            MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRGCPA-ASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                             GPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLV 166
 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKK1GLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                AVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT
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1 Similarity 98.5%;
321; Conservat'
                                                          Similarity
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G., X
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372 AA; 4
                                              49.3%;
larity 99.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                             AA;
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                                                                                             26934 MW;
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Pred.
2; M
                                              Pred.
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                                                                     Score
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                                                                                             A21C863E CRC32;
                                              re 1577; DB 4; I
1. No. 0.00e+00;
Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2451; DB 4;
No. 0.00e+00;
                                                                                                                                                                                                     COWPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC32;
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                                                                   Length 253;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                         000278
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01-JAN-1998
01-NOV-1999
SOLUBLE DEAT
                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUV-1998 (TrEMBLrel. 08, Last annotation update)
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 7.
"LARD: a new lymphoid-specific death domain regulated by alternative pre-mRNA splicing."
                                          SEQUENCE FROM N.A.
MEDLINE; 97272273.
SCREATON G.R., XU X.N., OL
MCMICHAEL A.J., BELL J.I.;
FLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF026071; AAB82288.1; -.
HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR_1;
PFAM; PF00020; TNFR_C6; 2.
SEQUENCE 277 AA; 29111 MW;
                                                                                                                                                           Eutheria; Primates;
                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           014866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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l Similarity 99.5%;
l81; Conservative
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-1998 (TrEMBLrel. 05, I
-1999 (TrEMBLrel. 12, I
E DEATH RECEPTOR 3 BETA
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                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                         Catarrhini;
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                                                                       OLSEN
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Pred. No. 2.10e-289;
1; Mismatches 0;
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Last annotation updat
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                                                                       A.L.,
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    splicing.";
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Best Local
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019131;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE; 97272273.

MEDLINE; 97272273.

SCREATON G.R., XU X.N., OLSEN A.L., COWPER A.E., TAN R.,

MCMICHAEL A.J., BELL J.I.;

TLAED: a new lymphoid specific death domain containing receptor regulated by alternative pre-mRNA splicing.";

Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).

ENBL; U94507; AAC51312.1;

ENBL; U94507; AAC51312.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000277
Eukaryota; Metazoa; Chordata; Eutheria; Cetartiodactyla; Ru Boyinae; Bos.
                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation updat
TUMOR_NECROSIS FACTOR-RECEPTOR I.
                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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EMBL;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYMPHOCYTE ASSOCIATED RECEPTOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                152 RLLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                              107 RLLC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113
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Local Similarity 100.0%;
Local Similarity 100.0%;
es 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 151
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U94508; AAC51313.
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59; Conser
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                                                                                          (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; death; 234 AA; 2
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larity 92.2%;
Conservative
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25373 MW;
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.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 467; DB 4; Len
Pred. No. 4.18e-72;
                                        :a; Craniata;
Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1329;
Pred. No. 1.
0; Mismatc
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. No. 1.37e-267;
Mismatches 0;
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                                        Vertebrata; Mammalia;
Pecora; Bovoidea; Bovi
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                                             Bovidae;
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Best Local :
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                                               EMBL; AF018253; AAB86809.1; Receptor. SEQUENCE 616 AA; 66033 M
                                                                                                               GALIBERT L.;
"A homologue of the TNF receptor and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 98032977.
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90937; AAB65143.1; -.
HSSP; P19438; 1TNR.
HSSP; P19438; 1TNR.
PROSITE; P500652; TNFR.NGFR_1; 3.
PFAM; PF00531; death; 1.
PFAM; PF00531; death; 1.
PFAM; PF00020; TNFR_C6; 3.
SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;
                                                                                                                                                                                                           TOMETSKO
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TISSUE=AORTA;
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Local Similarity 30.0%;
nes 128; Conservative
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    Match
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                                                                                                                                                                               D.M., MARASKOVSKY E., M.E., ROUX E.R., TEEP
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                                            66033 MW;
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12, Last sequence update)
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79; 1
Score
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Pred. No. 3.50e-31;
                                                                                                                                                                                                                                                                                                                                                                                                               FACTOR-KAPPA B.
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                                                                                                                                                                                                    BILLINGSLEY W.
E M.C., DUBOSE
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Length
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616;
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TAKAGI M., TAKAHASHI H., KABEYA H., O
TAKAGI M., TAKAHASHI H., KABEYA H., O
"Cloning of sheep fas antigen.";
Submitted (MAR-1998) to the EMBL/GenB
EMBL; AB011671; BAA37093.1; -
HSSP; P25445; 1DDF.
PROSITE; PS00652; TNFR_NGFR_1; 1
SEQUENCE 327 AA; 36928 MW; 67261B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999
01-MAY-1999
01-NOV-1999
FAS PROTEIN.
                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097530
097530;
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097491;
Receptor.
NON_TER
                                                                                    "Canine tumor necrosis factor Submitted (JUL-1997) to the ENERL; AF013955; AAD01516.1; -HSSP; P19438; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
Eutheria; (
                                                                                                                                                                                                      DUTHIE S., NASIR L.,
                                                                                                                                                                                                                                    TISSUE=BRAIN;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                         PROSITE;
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Cetartiodactyla; Run
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                                                                                                                                                                                                      ARGYLE D.J., ECKERSALL P.D.
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Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                             or receptor, partial EMBL/GenBank/DDBJ da
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Pred. No. 1
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Mismatches 72;
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.27e-20;
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                   Q95185 PRELIMINARY; PRT Q95185; Q95185; Creat Q1-FEB-1997 (TrEMBLrel. 02, Creat Q1-JUN-1998 (TrEMBLrel. 06, Last Q1-NOV-1999 (TrEMBLrel. 12, Last TUMOUR NECROSIS FACTOR RECEPTOR F
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TNFR-1.
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Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata,
Eutheria, Rodentia, Sciurognathi, Murida
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RECEPTOR ACTIVATOR OF NF-KAPPAB (RANK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
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MGI:1314891; Infrsf11a.
pe00020; INFR_c6; 3.
ENCE 625 AA; 66621 MW
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M.E., ROUX E.R., TEEP
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                   Last sequence update)
Last annotation update)
PTOR P60 (FRAGMENT).
                                                                                           Created)
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Pred. No. 1.74e-19;
30; Mismatches 69
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Pred. No. 4.16e-19;
23; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BILLINGSLEY W.E M.C., DUBOSE
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Eukaryota;

Metazoa; Chordata;

Craniata;

Vertebrata;

Mammalia;

(Cat)

Felis silvestris catus

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Best Local Similarity 34.0%;
Matches 32; Conservative
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Best Local Similarity 31.8%;
Matches 49; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETO A.;

SOLUTIONO T., TANBE Y., NAGANO Y., SETO A.;

SPILICING and allelic variation in the rabbit Fas antigen gene.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; ABO21297; BAA78429.1;

SEQUENCE 263 AA; 30374 MW; 43BF129F CRC32;
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Q9XS60
PRELIMINARY; PRT; 263 AA.
Q9XS60;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
FAS ANTIGEN SPLICED VARIANT
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Lagomorpha; Leporidae; Oryctolagus.
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[1]
                                                                                                                                                                                                                                                                                                 100 VETD-CTTIQNTKCRCKSNFF--CNALKCEHCDP 130
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                                                                                                                                                                                                                                102 VALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 135
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Pred. No. 1.31e-17;
19; Mismatches 37;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1254
1 ATGGAGCAGCGCGCGGGG......GCCTGCAGCGCGCGCCCGTGA 1254
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

AF134858 Mus muscu	AF134858	12	18015	17.3	217.4	c 24	
AL158217 Homo sap	AL158217	40	121345	26.4	331.4	23	
U83599 Human alter	HSU83599	11	651	27.3	342.2	22	
U94507 Human lympl	HSU94507	11	838	40.7	510.4	21	
U75381 Human apopt	HSU75381	11	808	42.0	526.4	20	
U83598 Human death	HSU83598	11	816	42.1	527.4	19	
U94512 Human lympl	HSU94512	11	809	42.7	535.4	18	
U94508 Human lymp)	HSU94508	11	705	43.7	547.8	17	
U94506 Human lympl	HSU94506	11	952	50.2	630	16	
U94505 Human lympl	HSU94505	11	1087	72.6	910	15	
U94509 Human lympl	HSU94509	11	1119	77.7	974	14	
U94510 Human lymph	HSU94510	11	1143	81.5	1022	13	
AF026071 Homo sap	AF026071	11	1763	88.0	1103.4	12	
U94504 Human lympl	HSU94504	11	1198	90.3	1132	11	
Y09392 H.sapiens m	HSWSL1	9	1743	90.4	1133.4	10	
U94503 Human lymph	HSU94503	11	1355	91.1	1143	9	
AF026070 Homo sapi	AF026070	11	1669	95.5	1197.4	œ	
U75380 Human apopt	HSU75380	11	1557	98.4	1233.8	7	
U83597 Human deatl	HSU83597	11	1528	98.5	1234.8	6	
2 Human	HSU94502	11	1257	99.0	1241	5	
U74611 Human Apo-	HSU74611	11	1634	100.0	1254	4	
U94501 Human lymph	HSU94501	11	1254	100.0	1254	ω	
U78029 Human aoptc	HSU78029	11	1254	100.0	1254	2	
U72763 Human death	HSU72763	11	1254	100.0	1254	ш	
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                                                                                                                                                                                                            Submitted (29-SEP-1996) Pathology, University of Michigan Medical School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA Location/Qualifiers
                                                                                                                                                                                                                                                    2 (bases 1 to 1254)
Chinnaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M., Duan, R., Xing, L., Gentz, R., Ni, J. and Dixit, V.M.
                                                                                                                                                                                                                                                                                                                                                                                                         Human death receptor U72763 U72763.1 GI:1669511
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1 (bases 1 to 1254)
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/db_xref="taxon:9606"
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A29098 Synthetic D
A20255 55kD recept
A21522 TNF alpha 9
I43805 Sequence 24
M33294 Human tumor
A26412 cDNA for (5
M58286 Homo sapien
M63121 Human tumor
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164751 Sequence 1
A19907 Synthetic n
M75866 Human tumor
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A43873 Sequence 1
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961 CCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGGCCCGCAGCTCTACGACGTGATGGAC 1020
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	1020	961 CCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGGGCCCGCAGCTCTACGACGTGATGAAC	o <sub>y</sub>
	960	901 GACCAGTTGCCCAGCAGAGCTCTTGGCCCCGCTGCTGCGCCCACACTCTCGCCAGAGTCC	Оу
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	780	721 ATGGAGGCTCTGACCCCACCGCCACCGCCATCTGTCACCCTTGGACAGCGCCCACACCC	Qy Db
	3 720 3 720	661 ACCTACACATACCGCCACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGG	Оу
	660	601 TTCTGGGTCCAGGTGCTCCTGGCTGGCCTGTGTGGTCCCCCTCCTGCTTGGGGCCACCCTG	Qу
	600	541 ACGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGT	Qy Db
	540	481 GACTGTGGGACCTGCCTGCCTGCCTTCTATGAACATGGCGATGGCTGCCTGTCCCCCCCC	Оy
•	480	421 TGCCTAGACTGCGGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACT	Qy
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	360	301 CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGC	Qy Db
	C 300 C 300	241 TGGGAGAACCACATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTC	ОУ
	240	181 TGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCAAGACACCTTCTTGGCC	Qy
	180	121 AAGAAGATTGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCT	Qу
	120	61 GGGCCCGGGCCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCAC	Qy
	60	1 ATGGAGCAGCGGCCGGGGGCTGCGCGGCGGTGCGGGGGGGG	Qy
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/protein_id="AAC51306.1"
/protein_id="AAC51306.1"
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/db_xref="G1:2071949"
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DCGTCLLGFYBHGDGCVSCPTSTLGSCDERCAAVCGWRQMFWVQVLLAGLVYPLLJGA
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/codon_start=1
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/db_xref="taxon:9606"
/cell_line="HeLa"
/cell_type="lymphocyte"
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Submitted (15-OCT-1996) Molecular Oncology, Genentech,
Submitted (15-OCT-1996) Molecular Oncology, Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marsters, S.A., Sheridan, J.P., Goddard, A.D., Bauer, K.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1634)

Marsters, S.A., Sheridan, J.P., Donahue, C.J., Pitti, R.M., Gr Goddard, A.D., Bauer, K.D. and Ashkenazi, A.

Apo-3, a new member of the tumor necrosis factor receptor contains a death domain and activates apoptosis and NF-kB
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Location/Qualifiers
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TNF receptor family member"
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                                                                                                                                                                                                                                                                                                                                                                                                    Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.

LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
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Submitted (19-MAR-1997) Molecular I
Molecular Medicine, John Radcliffe
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1 (bases 1 to 1257)
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/protein id="AAC51307.1"
/db_xref="G1:2071951"
/db_xref=
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Accession Number U94501, probably rep
3 splice site"
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/codon_start=1
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/db_xref="taxon:9606"
/cell_line="HeLa"
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Pred. No. 3.8e-202;
); Mismatches 0;
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ORGANISM

Homo sapiens

Human dea U83597 U83597.1

GI:1800292 domain 1528 dq receptor mRNA w (DDR3)

HSU83597 Human death

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 1528)
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/product="death domain receptor 3"
/product="Ash41432.1"
/protein_id="Ash41432.1"
/db_xref="G1:1800293"
/db_xref="G1:1800293"
/db_xref="G2:1800293"
/db_xref="G2:18
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/function="mediates apoptosis when cross-linked"
/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
/note="A TNFR1-related death-domain containing recepto
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Primates; Catarrhini; Hominidae; Homo.
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99.8%;
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Pred. No. 4.1e-201;
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U75380.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1557)

Bodmer,J.L., Burns,K., Schneider,P., Hofmann,K., Steiner,V.,

Thome,M., Bornand,T., Hahne,M., Schroter,M., Becker,K., Wilson,A.,

French, L.E., Browning,J.L., MacDonald,R. and Tschopp,J.

TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)

Immunity 6 (1), 79-88 (1997)
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Submitted (18-OCT-1996) Institute of Biochemistry, University Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1557)
Bodmer, J.L., Burns, K.,
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SWTPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYD
VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Translation="AAAGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFC
CRGCPAGHYLKAPCTEDCGNSTCLVCPDTFTLAWENHHRSECAAHGQACDEQASQVALE
NCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLLCGALHRHTRLLCARRDTDCG
TCLLGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLT
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<1. .1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="apoptosis-mediating receptor TRAMP"
/protein_id="AAC51192.1"
/db_xref="GI:1695925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="fetal lung"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="mediates apoptosis"
/note="contains a death domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="activates NF-kB"
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Pred. No. 6.1e-201;
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MEDLINE REFERENCE DEFINITION ACCESSION REFERENCE SOURCE ORGANISM JOURNAL AUTHORS AUTHORS æ Warzocha, K., Salles, G.
Direct Submis Warzocha, K., Ribeiro, P., Salles, G. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1669) Homo sapiens AF026070 Biochem. Biophys. A new death receptor 3 isoform: expression lines and non-Hodgkin's lymphomas Homo sapiens AF026070 98113360 AF026070 (bases 1 to Ribeiro, death receptor 1669) dq s lymphomas Commun. 24 Charlot, C., Renard, N., ω beta (2), (DR3) mRNA, Charlot, C., Renard, N., 376-379 complete Coiffier, B. Coiffier, B. Mammalia; cds. and and

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ALENCSAVADTRCGCRPGWFVECOVSQCVSSSPFYQDCLDGALHRHTRLLCSRRDT
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AMMLOPGPQLYDNMDAVPARRWKEFVRTLGLREAEIEAVEVEIGLFRDQQYEMLKHWR
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/protein_id="AAC39556.1"
/db_xref="GI:2570831"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1355)

Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.

LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

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Direct Submission
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/note="LARD-2; similar to Fas soluble; truncated before the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="insertion compared to LARD la, deposited in GenBank Accession Number U94501, probable retained intron leading to premature transcriptional termination" 441 c 451 g 240 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="lymphocyte associated receptor of death 2"
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92.5%;
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Pred. No. 1.8e-185;
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721	1 TGGCTGGCCTTGTGGTCCCCCCTCCTGCTTGGGGCCACCCTGACCTACACATACCGCCACT 780
680	
781	1 CTTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTCTGACCCCAC 840
740	
841	LACCGGCCACCCATCTGTCACCCTTGGACAGCGCCCACACCCCTTCTAGCACCTCCTGACA 900
800	- ၈
901	1 CCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTGGCTACCCCG
860	
961	AGACCCAGGAGGCGCTCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGCCCAGCAGAG 1020
920	CTCTTGGCCCCGCTGCTGCGCCCACACTCTCGCCAGAGTCCCCAGCCGGCTCGCCAGCCA
1021	1 CTCTTGGCCCGGCTGCTGCGCCACACTCTCGCCAGAGTCCCCAGCCGGCTCGCCAGCCA
980	TGATGCTGCAGCCGGGCCCGCAGCTCTACGACGTGATGGACGCGGTCCCAGCGCGCGC
1081	
1040	
1141	GGAAGGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGG
1100	AGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGC 115
1201	
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1261	1 CCGCGGGCCTCGGAGCCGTTTACGCGGGCCCTGGAGCGCATGGGGCTGGACGGCCTGCGTGG 1320
1220	
1321	` > -

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KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION VERSION HSWSL1 LOCUS REFERENCE TITLE JOURNAL MEDLINE AUTHORS Nature 384 97088617 Kitson,J., Raven,T., Jiang,Y.P., Goeddel,D.V., Giles,K.M., Pun,K.T., Grinham,C.J., Brown,R. and Farrow,S.N.
A death-domain-containing receptor that mediates apoptosis Nature 384 (6607), 372-375 (1996) Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1743) H.sapiens mRNA for WSL-LR, WSL-S1 and  $y09392\,$ Homo sapiens wsl-1 gene; WSL-1R Y09392.1 GI:1669690 1743 dq protein; WSL-S1 protein; WSL-S2 protein WSL-S2 proteins. Mammalia;

Eutheria;

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/number=3
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/number=2
667...767
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UYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGLFRDQ0YEMLKHWRQQQPAGLGA
                                                                                                                      /number=4
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/cell +vro="m"
                                                                                                                                                                                                                                                                    VYAALERMGLDGCVEDLRSRLQRGP"
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Centre, Gunnels Wood Road,
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l. .1742
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                                  Score 1133.4;
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GCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTGGCTACCCCG
                                                                                                                                                                                                                                  CACCGGCCACCCATCTGTCACCCTTGGACAGCGCCCACACCCTTCTAGCACCCTCCTGACA
                                                                                                                                                                                                                                                                                           GCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGGGATGGAGGCTCTGACCCCAC
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360 368 300 308 240

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Submitted (19-MAR-1997) Molecular :
Molecular Medicine, John Radcliffe
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LARD: a new lymphoid-specific death domain containing regulated by alternative pre-mRNA splicing Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1198)
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                                                                                           /note="deletion compared to LARD la, deposited in GenBan
Accession Number U94501, probable skipping of putative
exon 6 leading to premature transcriptional termination"
405 c 384 g 216 t
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                                                                                                                                                                                                                                                                                                                                                               /function="mediates apoptosis"
/note="LARD-3; similar to Fas a
/note="LARD-1; truncated before the t
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/protein_id="AAC51309.1"
/protein_id="AAC51309.1"
/db_xref="Gi:2071955"
/translation="MEORPRGCAAVAAALLLVILGARAOGGTRSPRCDCAGDFHKKIG
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                                                                                                    ATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAG
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Submitted (19-SEP-1997) Hematology, CTRE Hospitalier
Chemin du Grand Royoyet, Pierre Benite 69495, France
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1 (bases 1 to 1763)
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DCGTCLPGFYEHGDGCVSCPTPPSLAGAPWGAVQSAVPLSVAGGRVGCVLGMRVGEL
GWTEGRRVRRGATTQHPPAAFSVLGPGAPGWPCGPPPAWGHPDLHIPPLLASQAPGYC
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                                                                                                                                                                                                                                                                                                                                                                                              /product="soluble death receptor 3 beta"
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/translation="Megrprecopto"
/translat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="sDR3 beta; TNF receptor family member; alternatively spliced product; lacks transmembrane due to insertion of 95 nucleotides from exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identified in human pre-B cell line
patients with non-Hodgkin's lymphoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/note="identified in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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Direct Submission
Submitted (19-MAR-1997) Molecular Immunology
Submitted (19-MAR-1997) Molecular Immunology
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LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
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U94510
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/note="LARD-9; NGFR
TNF-R1"
                                                                                                                               /note="deletion compared to LARD 1a, deposited Accession Number U94501, probable skipping of person 7 encoding the transmembrane domain" 378 c 378 g 199 t
                                                                                                                                                                                                                                                    /product="lymphocyte associated receptor of death 9"
/protein_id="AAC51315.1"
/db_xref="G1:2071967"
/tanslation="MEQRPRGCAAVAAALLLYLLGARAQGGTRSPRCDCAGDEHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQV
ALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDT
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PTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRF
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                                                              CTTCTAGCACCTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGC
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screaton, G.R., Xu, X.N., Olse McMichael, A.J. and Bell, J.I.
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/protein_id="AAC51314.1"
/protein_id="AAC51314.1"
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                                                                                                                                                                                                                                                                                    /note="deletion compared to LARD 1a, deposited in GenBank Accession Number U94501, probable skipping of putative exon 3\,\mathrm{''}
                                                                                                                                                                                                                                                                                                                                               AGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP"

160. .161
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TNF-R1"
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/db_xref="taxon:9606"
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Medicine, John Radcliffe
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/note="LARD-8; NGFR family member;
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Pred. No. 1.1e-156;
0; Mismatches 0;
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960 765 900 705 840 645 780 585 720 525 660

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TITLE
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Best Local Similarity
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spliced, output
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U94505.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screaton, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., McMichael, A.J. and Bell, J.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1087)
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542. .543
                                                                                                                                                                                                                                                                                     termination"
                                                                                                                                                                                                                                                                                                /note="deletion compared to LARD la, deposited in GenBank Accession Number U94501, probable skipping of putative exons 6 and 7 leading to premature transcriptional
                                                                                                                                                                                                                                                                                                                                                                                          /product="lymphocyte associated receptor of death 4"
/protein id="AAC51310.1"
/protein id="AAC51310.1"
/db_xref="GI:2071957"
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LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LARD-4; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="mediates apoptosis"
/note="LARD-4; similar to Fas
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/db_xref="taxon:9606"
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06-FEB-1997; US-037341.
12-MAR-1996; US-03281.
17-OCT-1996; US-028711.
17-OCT-1996; US-028711.
(HUMA-) (HUMAN GENOME SCI I (UMMI) UNIV MICHIGAN.
WPI; 99-124390/11.
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New death domain containing receptor and recombinant vector optionally comprising leader sequence claim 6; Fig 3; SUpp; Japanese.

The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents a cDNA encoding the death domain containing receptor polypeptide (DR3).

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Example 1; Page 45-46; 70pp; English.
CCDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see CHAR clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see TDIIS) and the mammalian cells. It was isolated from a human foetal CD activity in mammalian cells. It was isolated from a human foetal CD activity in mammalian cells. It was isolated from a human foetal CD activity in mammalian cells. It was isolated from a human foetal CD activity in mammalian cells actided to another novel apoptosis CD collect Polypeptide, Apo-3 are identical to another novel apoptosis CD produce recombinant Apo-3 polypeptides, especially the cacids 338-417). Apo-3 can be used to induce apoptosis or CD actides another actided the actided containing cells that the purposes. Non-human transgenic animals containing cells that colline that the produce actided and knockout animals containing cells that the produce actided act
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Best Local Similarity
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23-SEP-1996; US-710802.
01-APR 4996; US-625328.
(GETH) GENEWTECH INC.
Ashkenazī AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1997;
31-MAR-1997;
23-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells that have an altered Apo-3 gene, can be used in drug screening and development.
Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T
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09-APR-1998.
03-OCT-1997; U17876.
04-OCT-1996; UB-044456.
(IMMV \ IMMUNEX-CORP.
Perkins PA.
                                                                                                                                                                                                                                                                                                                                                              Human apoptosis inducing receptor coding sequence. Apoptosis inducing receptor; AIR protein; human; c Type I transmembrane protein; tumour cell death; a
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WPI; 98-240077/21.
P-PSDB; W57045.
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Best Local Sim
Matches 1254;
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This sequence encodes the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases. Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T;
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ATGGAGGCTCTGACCCCACCACCGGCCACCCATCTGTCACCCTTGGACAGCGCCCACACC
                                                                                                               ACCTACACATACCGCCACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGG
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1.6e-263;
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              to treat inflammatory diseases

Claim 2; Page 71-73; 108pp; English.

This cDNA clone, deposited as ATCC 97456, codes for human death domain containing receptor DR3 VI (see W31516), a novel member of the tumour necrosis factor receptor family. It was isolated from a CDNA library derived from cells of a human testis tumour. Related death domain containing receptor DR3 cDNA (see T8942)) was isolated from a HUVEC cDNA library. The genes have also been identified in CDNA libraries of foetal lyre foetal brain, tonsil and leukocyte. Nucleic acids encoding full-length or mature DR3-VI can be used to produce recombinant polypeptides in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the inhibition of apoptosis. Antagonists, such as antibodies raised against DR3-VI, can be used to treat diseases and disorders associated with increased apoptosis and for treating inflammatory
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(UNMI) UNIV MICHIGAN.
Dillon PJ, Dixit VM, G
WPI; 97-470812/43.
P-PSDB; W31516.
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17-OCT-1996; US-013285.
12-MAR-1996; US-013285.
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12-MAR-1997. US-037341.
12-MAR-1996. US-013285.
17-OCT-1996. US-028711.
(HUMA-) HUMAN GENOME SCI I.
(UNMI) UNIV MICHIGAN.
WPI, 99-124390/11.
P-PSDB; W95537.
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Key
CDS
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Claim 2; Fig 1, 2; 50pp; Japanese.
The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 9757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents a cDNA encoding the death domain containing receptor polypeptide (DR3-V1).

Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T;
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Pred. No. 4.2e-255;
0; Mismatches 8;
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DR3; recombinant; ds.
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This sequence encodes the mouse apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases. Sequence 1251 BP; 224 A; 390 C; 375 G; 262 T;
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Key
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09-APR-1998.
03-OCT-1997; U17876.
04-OCT-1996; US-0444456.
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Mouse apoptosis inducing receptor coding a
Apoptosis inducing receptor; AIR protein;
Type I transmembrane protein; tumour cell
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            CTGTGGCTGTAAGCCAGGCTGGTTTGTGGAGTGCCAGCTCAGCCAATGTGTCAGCAGTTC
                                                                                                                                        CTGTGATGAAGAGGCCCTTCAAGTGACCCCTTGAGAACTGCTCGGCAAAGTCGGACACCCA
                                                                                                                                                       CTGTGATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCG
                                                                                                                                                                                                         CCAAGACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCTGCCAGGC
                                                                                                                                                                                                                                            GCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTCC
                                                                                                                                                                                                                                                                                             GCTCCTCCTGGTGCTGCTGGGGGCCCGGGCCCCAGGGCGCACTCGTAGCCCCCAGGTGTGA 101
                                      ACCTTTCTCTTGTGTCCCATGC-----
                                                                                        CTGTGGCTGCCAGTCAGGCTGGTGTGTTGACTGCTCCACCGAGCCATGTGGGAAAAGCTC
                                                                                                                                                                                           GCTGCTGCTGCTGCTTGGTGGCCAGGGCCAGGGCGGCATGTCTGG----CAGGTGTGA
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73.8%;
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Pred. No. 2.7
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-GGGGCTACAACACCAGTCCATGAGGCT
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nes 276;
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14-APR-1998 (first entry)
Human apoptosis protein Apo-2LI cDNA clone Apo-2LI; apoptosis; Apo-2 ligand inhibitor;

T91179

standard;

CDNA;

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W09737020-A1 09-OCT-1997.

mat\_peptide

sig\_peptide

/\*tag= a 377. .436

/\*tag=

Location/Qualifiers 377. .922

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hydropathy

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                                                                                                                                                                                                                                                                                                                                  GCTGGGGCTGCGCGAGGCAGAGCTCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCGAGA
                                                                                                                                                                                                                                                                                                                                                                                          ATCTCCGCTCTCGCCAGCGCCCCCTGCGGGCTCTCCGGCTGCTGCTCCAGCCTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGACAGGCCTCACAACCCTGGGATCAGCTGCCAAACAGAACTCTTGGAACTCCTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCCAGTTGGTAGGCAACAACTGGACCCCTGGCTTATCCCAGACTCAGGAGGTGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCTTGGGGCCACCCTGACCTACACATACCGCCACTGCTGGCCTCACAAGCCCCTGGT
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RESULT
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CDNA clone 18.1 (ATCC 97493) codes for a novel polypeptide (see CDNA clone 18.1 (ATCC 97493) codes for a novel polypeptide (see CDNA clone 18.1), that can be was isolated from a human thymus cDNA library by screening with probes (see T91181-82) based on an EST sequence (GenBank locus probes (see T91181-82) based on an EST sequence (GenBank locus 414522) that showed homology to human Fas/Apo-1. The clone encodes an Apo-2LI polypeptide that is identical to amino acid residues to an apo-2LI polypeptide that is polypeptide, Apo-3 (see W26709), but appears to represent a naturally-occurring mRNA. Nucleic acids encoding Apo-3 (see T91180) or Apo-2LI can be used diagnostically for tissue-specific typing and can be used to produce the recombinant polypeptides including chimeric molecules comprising polypeptides fused to heterologous amino acid sequences.

Sequence 1438 BP; 287 A; 392 C; 469 G; 290 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 547; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1997; U05230.
23-SEP-1996; US-710802.
01-APR-1996; US-625328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide(s) Apo-3
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                                                        917
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                                                                                                                                                                                                                                                                                                                                   GGGGCCCGGGCCCAGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                          TGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAGATTGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCT
                                                                                                                           GACTGTGGGACCTGCCTGCCTTGCTATGAACATGGCGATGCCTGCGTGTCCTGCCCC
                                                                                                                                                                                                                                                                                                                                                                                           TGCACGGAGCCCTGCGCAACTCCACCTGCCTTGTGTGTCCCCAAGACACCTTCTTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAGATTGGTCTGTTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCT
                                                        ACGTAATTCCTAG
                                                                                  ACGAGCACCCTGG
                                                                                                              GACTGTGGGACCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCCTGCCCC
                                                                                                                                                                     TGCCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACT
                                                                                                                                                                                TGCCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACT
                                                                                                                                                                                                                         TGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Apo-2LI - useful for regulating apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 543.4; DB 1;
Pred. No. 2.7e-109;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The clone encodes
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Best Local s
Matches 128
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26-MAR-1993;
30-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; page 57-59; 85pp; English. The sequences given in 049931-32 encode human tumour necrosis fact receptor (TNF-R) and the sequences in 049933-34 encode human interleukin-1 receptor (IL-IR). These sequences were used in the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
                                                                                                                                                                                                                                                                                                                   The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moeities by such a distance that each component of the fusion protten is capable of folding into the secondary or tertiary structure required for its biological activity. These fusion proteins may be used in therapy, diagnosis and assays for conditions mediated by TNF or IL-1, particularly in conditions in which both TNF and IL-1 play a causitive role. They may be used to treat cachexia, rheumatoid arthritis, cerebral malaria, allograft and xenograft rejection in graft verses host disease, sepsis, septic shock, inflammation, allergies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF-R-linker-TNF-R-linker-TL-1R
IL-1R-linker-TNF-R-linker-TNF-R
TNF-R-linker-TNF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1993; U02938.
30-MAR-1992; US-860710.
(IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune dysfunction; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft verses host disease; sepsis; inflammation; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q49932;
29-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q49932 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith CA;
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                                                                                                                                                                                                                                                                                                          autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cormulae:
                                                                                                                                                                                                                                                                                       oral mararry, disease, sepsis, septro commune dysfunctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93-336592/42.
DB; R42059.
CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGCTGCGTGGAAGACT
                                                                                                           CACGCTGGGGGCTGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG
                                                                                                                                                                                    AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCCGGGGCCTCGGAGC
                                                                                             GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT
                                                                                                                                                       Similarity
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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121. .1363
/*tag= c
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                                                                                                                                                                                                                                5.3%;
55.7%;
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                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                Score 66.8;
Pred. No. 3
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                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                               424
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                                                                                                                                                                                                                                 ; DB 1;
3.8e-06;
                                                                                                                                                                                                                                                                                               376
                                                                                                                                                                                                                     102;
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                                                                                                                                                                                                                                                 Length 1368;
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RESULT 11
Q24440
ID Q24440
AC Q24440
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                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  New tumour necrosis factor alpha binding protein and polypeptide - useful in treating cachexia, sepsis and auto immune diseases e.g. rheumatoid arthritis
Disclosure; Fig 1; 25pp; English.
The sequence is that of DNA encoding tumour necrosis factor alpha binding protein which was obtd. from a human placental cDNA library in lambda gtll using a probe (020974). The DNA also encodes the extracellular domain of human TNF alpha receptor and as such it is useful for treating diseases where TNF alpha is involved as a causative agent, e.g. cachexia, sepsis and autoimmune diseases, specifically rheumatoid arthritis. See also Q20974.
Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;
                                                                                                                                                                                                                                                                                                                                                                                                    GB2246569-A.
05-FEB-1992.
15-JUN-1990;
15-JUN-1990;
Q24440 standard;
Q24440;
                                                                                                                                                                     1222
                                                                                                                                                                                                                                                                                                                                                                         (CHAR-) CHARING CROSS SUNLE.
Feldman M, Gray P, Turner M, Brennan F;
WPI; 92-043613/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis
extracellular do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF-alpha binding protein gene Tumour necrosis factor alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q20973 standard; DNA; 2062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1248 CACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCT 1297
                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R20787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1992
                                                                                                    AGACCAGCAGTACGAGATGCTCAAGCGCTGGGGGCCAGCAGCAGCAGCCGGGGGCCTCGGAGC
                                                                                                                                        CACGCTGGGGCTGCGCGAGGCCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG
                                                                                                                                                                  CACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCT
                                                                       CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGGCTGCGTGGAAGACT 1225
                                                                                          GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT
                                                                                                                                                                                   sapiens
                                                                                                                                                                                                       Conservative
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GB-013410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
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473. .532
        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
/note= "homologous to probe Q20974"
242. .751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encodes the TNF alpha receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                               5.3%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 274
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         2062 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                       0;
                                                                                                                                                                                                      Score 66.8; DB 1;
Pred. No. 4.1e-06;
0; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune diseases; cachectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular domain
                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                       102;
                                                                                                                                                                                                                        Length 2062;
                                                                                                                                                                                                       Indels
                                                      1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human
                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                          library
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treating autoimmune disease, septic shock, HIV etc.

Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA library in 9t10 was screened with probe Q29236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The inserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF-alpha C5kD receptor was isolated as an EcoRI fragment encoding 374 amino acids, and cloned into a mammalian cell expression vector, resulting in prTNFR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane domain. PCR with primers Q29237,8 generated a 300bp restriction fragment which was cloned into prTNFR, giving pTNFRecd. DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.
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                                                                                 1342
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18-OCT-1991;
18-OCT-1990;
1176 CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGGCTGCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHAR-) CHARING CROSS SUNLEY Brennan FM, Feldmann M, Gray WPI; 92-167156/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria; viral meningits; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encodes Tur-alpha 55kD receptor.

Encodes Tur-alpha 55kD receptor.

tumour necrosis factor alpha; extracellular binding domain; tumour necrosis factor alpha; tumour necrosis factor alpha; extracellular binding domain; tumour necrosis factor alpha; tumour necrosis factor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide capable of binding human TNF alpha - compr
first three cysteine-rich subdomains of TNF alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; R24000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                       signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                CACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG
                                                                                                                                                                                                                                                                                                                                                                        GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT
                                                                                                                                                       AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCCCGCGGGCCTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q24440-51, R24000, R24080-84, R27585, 2062 BP; 429 A; 618 C; 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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/codon= seq:"TGG",
1258. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon= St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
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1265. .126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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55.7%;
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on= Seq"AAG",
. .1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۵
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66.8; DB 1;
Pred. No. 4.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q29236-8
G; 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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   1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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1402 CACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCT 1451

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Best Local S
Matches 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-1989; US-381080.

11-DEC-1989; US-450329.

07-FEB-1990; US-479661.

(SYNE-) SYNERGEN INC.

WPI; 91-073847/11.
                                                                     Oluso;
24-MAY-1991 (first entry)
Encodes human 55kD TNF-binding proteins; septic shock;
Tumour Necrosis Factor; binding proteins; septic shock;
                                                                                                                                                                                                                                                     1296
                                                                                                                                                                                                                                                                        1056
                                                                                                                                                                                                                                                                                           1236
                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence encodes the entire 30 kD TNF inhibitor. The clon which the sequence was obtd. was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The way
 EP-417563-A.
20-MAR-1991.
                                                                                                                                                                                                                                                                                                                                                                                See also Q10878, Q10884 and Q10907. Sequence 2088 BP; 439 A; 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and -beta, useful as therapeutic agent.
Disclosure; Fig 21; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           010883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q10883 standard; cDNA; 2088
                                       mat_peptide
                                                          signal_peptide
                                                                                                                            Q10955 standard;
                                                                                                                                                                           1416 CACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCT 1465
                                                                                                                                                                                                                                   1116
                                                                                                                                                                                                                                                                                                                                                                                                   diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R10986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1991.
16-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU9058976-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30kD TNF inhibitor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                           inhibitor for use in the treatment of inflammatory and
                                                                                                                                                                                                                                                                                                              996
                                                                                                                                                                                                                                                                                                                                Local Similarity
mes 128; Conserv
                                                                                                                                                                                                                                                                 CACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG
                                                                                                                                                                                                                                                                                                            can be inserted
                                                                                                                                                                                              CGTTTACGCGGCCCTGGAGCGCCATGGGGCTGGACGGCTGCGTGGAAGACT
                                                                                                                                                                                                                                  AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCCAGCAGCAGCCCGCGGGCCTCGGAGC
                                                                                                                                                                                                                                                      GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT
                                                                                                                                                                                                                                                                                           GCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCGCACGCCGCGGCGCGAGGC
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                           Location/Qualifiers 187. . 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 171. .1536
                                       274.
                     /product= 55kD TNF-BF
                               /*tag=
                                                                                                                            cDNA;
                                               /*tag=
                                       .1551
                                                                                                                                                                                                                                                                                                                                         5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      into expression vectors for prepn.
                                                                                                                            2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΒP
                                                                                                                                                                                                                                                                                                                               Score 66.8; DI Pred. No. 4.1e. 0; Mismatches
                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene in lambda-gt10-7ctnfbp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for suppression of TNF-alpha
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                                                                                                                                                                                                                                                                                                                                         8; DB 1;
4.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                578
                                                                                                                                                                                                                                                                                                                                 102;
                                                                                                                                                                                                                                                                                                                                                                                <u>و</u>;
                                                                                                                                                                                                                                                                                                                                                    Length 2088
                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            degenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                      of TNF
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                                                                                                                                                                                                                                                                                                                                                                                                                               whole
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                   RESULT
Q06285
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brockhaus M,
Schlaeger EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insoluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                         Key
                                                                                                                                                                                                                 006285
                                                                                                                   EP-393438-A.
                                                                                                                                                                  Homo
                                                                                                                                                                                                                            006285
                                        P-PSDB; R07451
                                                                                                                                                                                                         29-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                              996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Improved
                                                                                                                                                                            .ambdaTNF-R2;
                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                128;
                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R11082.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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   (Q06284) was
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prodn.
Claim 4; Fig 1; 26pp; German.
Claim 4; Fig 1; 26pp; German.
Partial amino acid sequences were determined for the 55 and 75kD
Partial amino acid sequences were determined for the 55 and 75kD
Partial amino acid sequences were used
TNF-BPs (see R11072-R11081) and oligonucleotide primers were used
synthesised based on these partial sequences. The primers were used
to produce a cDNA fragment for use as aprobe to screen a human
to produce a cDNA constructed in lambda gtll. Positive clones were
placental cDNA bank constructed in lambda gtll. Positive clones were
placental cDNA bank constructed in lambda gtll. Positive clones were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifed and sequenced. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-AUG-1990; 116707.
12-SEP-1989; CH-003319.
08-MAR-1990; CH-000746.
20-APR-1990; CH-001347.
            tumour treatment and to understand mechanismsm Disclosure; Fig 91(1-2); 51pp; German.
                                                                                                                 24-OCT-1990.

06-APR-1990; 106624.

21-APR-1989; DE-913101.

21-JUN-1989; DE-920282.

(BOEH ) BOEHRINGER INGELHEIMINT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF ) HOFFMANN-LA ROCHE Brockhaus M, Dembic Z, Ger
                                                                                  Hauptmann R, Himmler A, WPI; 90-321987/43.
                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor binding
                                                                                                                                                                                                                                                                                                                                                    Human Tumour Necrosis Factor-Receptor cDNA insert
                                               DNA encoding TNF binding protein and TNF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGCAGCTCTACGACGTGATGGACGCGGTCCCAGCGCGGCGCGCTGGAAGGAGTTCGTGCG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT
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                                                                                                                                                                                                                                                                                                                   raTNF-R8;
                                                                                                                                                                                                                                                            Location/Qualifiers 213. .1577
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Pred. No. 4.1e
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                                                                                                                                                                                                                                                                                                                                    TNF-BP;
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HS913T
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See also Q06282-Q06285.
Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T;
                                   repeat_unit
                                                                                                 repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type I TNF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2-SEP-1991 (first entry)
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                /number= :
634. .756
/*tag= k
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/note= "TBP-I
889..957
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583. .627
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505. .633
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256. .318
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/note= "may be 2 codons
longer"
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Pred. No. 4.1e-06;
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Best Local Similarity
Matches 128; Conserv
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(YEDA ) YEDA RES & DEV CO LTD.

WALLach D, Nophar Y, Kemper O. F

Aderka D;
                                                                                                                                                                                                                                                                                    Recombinant tumour necrosis factor binding protein I - prepd. by transfecting eukaryotic cells with vector contg. deoxyribonucleic acid encoding human type T TNF receptor or soluble domain Disclosure; Fig 1(D); 30pp; English.

The Tumour Necrosis Factor Binding Protein I is the soluble form o type I TNF-receptor and constitutes a fragment of the cell surface form of this receptor, corresp. to its extracellular domain. There is no characteristic poly(A) addition signal near the 3' end of the cDNA. The sequence ACTAAA (tag m) may serve as an alternative to this signal, but with low efficiency. See also Q12212-15.
                                                                                1116
                                                                                                             1383
                                                                                                                                      1056
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                                                                                                                                                              WPI; 91-186774/26.
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                        CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGAACACT
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                                                                                                                                     CACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG
                                                                                                                                                                            CCCGCAGCTCTACGACGTGATGGACGCGGTCCCAGCGCGGCGCTTGGAAGGAGTTCGTGCG
                                                                             AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGGCCTCGGAGC
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                          US-08-050-319B-24
US-09-166-038A-1
US-09-166-038A-1
US-08-321-668-1
US-08-321-668-1
US-08-32-6016-1
US-08-32-015-2
US-08-576-626A-2
US-08-537-002A-4
US-08-537-002A-4
US-08-537-002A-4
US-08-537-002A-4
US-08-537-002A-4
US-08-537-002A-4
US-08-690-471-1
US-08-690-471-1
US-08-845-988-7
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US-08-050-319B-24
                                                                                                                  US-08-050-319B-24
Query Match 5.3
Best Local Similarity 55.7
Matches 128; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                       MOLECULE TYPE:
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ALIGNMENTS

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Sequence 24, Application US/08050319B Patent No. 5633145
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APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                       nucleic acid
DEDNESS: double
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Palo Alto
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cDNA to mRNA
                                                                                                                                                                                                                                          US/08/050,319B
                                                                                                                                                   5150-0030
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Score 66.8; DB 1; Pred. No. 5.4e-07; 0; Mismatches 102;

Length 2062; Indels

0;

Gaps

0;

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US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
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                                                Matches 128;
                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-32: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
NFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/OFILING DATE: 10-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1176 CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGGCTGCGTGGAAGACT 1225
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STREET: 635 Brya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                Conservative
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                                                               5.3%;
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                                                             Score 66.8; DB 3; Pred. No. 5.4e-07;
                                              Mismatches 102;
                                                                           Length 2062;
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Patent No. 6007995
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                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (760) 603-3820 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brenda F. TITLE OF INVENTION: F
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1176 CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGGCTGCGTGGAAGACT 1225
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (760) 931-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 222
                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows N SOFTWARE: Microsoft Word 97
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: June 26,
                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                            CACGCTGGGGCTGCGCGCGCAGGCAGAGTCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG 1115
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                                                           AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCCGCCGCGGGCCTCGGAGC 1175
                                                                                                                                                         GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGGCGCTGCCT 1341
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IBM PC compatible
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US-08-321-668-1
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Best Local Sin
Matches 128;
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                                   1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA: IL 1C
APPLICATION UNMBER: IL 1C
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
1176 CGTTTACGCGGCCCTGGAGCGCATGGGGCTGGACGGCTGCGTGGAAGACT 1225
                                                                                                                     1056 CACGCTGGGGCTGCGCGAGGCCAGAGATCGAAGCCGTGGAAGCTGGAGATCGGCCGCTTCCG 1115
                                                                                                                                                                   REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                     996 CCCGCAGCTCTACGACGTGATGGACGCGGGGGGCGCTGGGAAGGAGTTCGTGCG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 2018633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 41.
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/321,668 FILING DATE: 12-OCT-1994
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                               GCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCCGCGGCGCGAGGC
                                                               AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCCAGCAGCAGCCCGCGGGCCTCGGAGC 1175
                                                                                                  GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT 1442
                                                                                                                                                                                                                                                      Similarity
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VARFOLOMEEV, Eugene
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Pred. No. 5.5e-07;
0; Mismatches 102;
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APPLICANT: BATKIN, MI
TITLE OF INVENTION: N
TITLE OF INVENTION: N
TITLE OF INVENTION: N
TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IL 10726
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: U
FILING DATE: 12-OCT-1
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                                                                                1056 CACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG 1115
                                                                                                                                 FEATURE:
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1443 GCGCGAGGCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCCACGCCGCGGCGCGAGGC
                               1116 AGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGGCCTCGGAGC 1175
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                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                GCGCCTAGGGCTGAGCGACCACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCT 1442
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VARFOLOMEEV, Eugene
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULES INFLUENCING THE SHEDDING
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                                                                                                                                                                                               Score 66.8; DB 2;
Pred. No. 5.5e-07;
0; Mismatches 102;
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1176 CGTTTACGCGGCCCTGGAAGCGCATGGGCTGGACGGCTGGAAGACT 1225

1503 CACGCTGGAGCTGCTGGGACGCGTGCTCCGCGACATGGACCTGCTGGGCT 1552

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                                                                                           Best Local Similarity 55. Matches 128; Conservative
                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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            1056 CACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCG 1115
                                       FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                      TELLEFAX: 202
TELEFAX: 248633
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LOCATION:
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REFERENCE/DOCKET NUMBER:
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E: Browdy and Neimark 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                            2175 base pairs
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ENGELMANN, HARTMUT
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                                                                                                                                                                      mat_peptide
319,.1620
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256..1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/126,016
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                                                                                                                                                                                                                                                                                                                                                                                                                    25,618
                                                                                                                                                                                                                                                                                                                                                                                                          WALLACH4
                                                                                           0;
                                                                                                      Score 66.8; DB 2;
Pred. No. 5.5e-07;
                                                                                             Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite
Length 2175;
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Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/2:
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ
                                                               1225
                                                                                                                               1165
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: 18-3000
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1503 CACGCTGGAGCTGCTGGGACGTGCTCCGCGACATGGACCTGCTGGGCT 1552
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 1285
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                                                                                                                                                APPLICATION NUMBER: FILING DATE: 09-DEC
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                                                                                                                                                                                                                                                                                                                                TYPE:
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GCGAGGCTCAGTACAGCATGCTGGAAGCCTGGCGGCGCGCCACGCC
                             GAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCC 1160
                                                               CGCTGGGGCTGCGCGAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCT---TCC 1114
                                                                                                                               CGATTCTGTATGCTGTGGTGGATGGCGTGCCTCCAGCGCGCTGGAAGGAGTTCATGCGTT 1224
                                                                                                                                                                                              al Similarity
106; Conserv
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DEDNESS: single
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                 ID NO:
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63.98;
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Flavia M.
MODIFIED RECEPTORS THAT CONTINUOUSLY
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                                                                                                                                                                                                0;
                                                                                                                                                                                              Score 58.8; DB 4; Pred. No. 3.7e-05; n: Mismatches 57;
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US-07-642-734C-3/c
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 17-JAN-91 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
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APPLICANT: Mcalpine, J B
                                                           FEATURE:
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NAME/KEY:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                     NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3'
                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 97..1482
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 19..4470 OTHER INFORMATION: /fur OTHER INFORMATION: modu
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                     NAME/KEY:
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LOCATION: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
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   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
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                   misc_feature
3406..3921
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Erythromycin Analogs
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                                                                                                                                                                       beta-ketoacyl
                                                                                                                                                                                                                                                                         module
                                                                                                                                                                                                                                                                                                                                                              /codon_start= 19
/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                       /function=
module 3"
/function= "approximate span of
                                                                                                                                                                                           /function= "approximate span of
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OTHER INFORMATION: OTHER INFORMATION: FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 14062..14610
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span o
OTHER INFORMATION: acyl carrier domain of module
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LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
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LOCATION: 9433..9984
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase of module
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                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 14857..15114
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LOCATION: 10723..20235
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LOCATION: 4471..5847
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                                          NAME/KEY: misc_feature LOCATION: 15166..20235
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10723..15165
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dehydratase and enoylreductase domains
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beta-ketoreductase of module
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beta-ketoacylACPsynhase domain
                                                                                                          acyl carrier
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acyltransferase domain of modul
/function=
module 6"
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module 5"
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/function= "gene =eryA"
/product= "orf3 encoding modules 5 &
6-deoxyerythronolide B formatio"
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                                                                                                       /function= "approximate span of
acyl carrier domain of module 5"
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                    "approximate span
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                                                                                                 US-08-232-015-2/c
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             Sequence 2, Application U
patent No. 5650272
GENERAL INFORMATION:
APPLICANT: GUESDON, J
APPLICANT: THIERRY, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Matcn
Best Local Similarity
Matches 199; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 GTTGGTGGGTAACAGCTGGACCCCTGGCTACCCCGAGACCCAGGAGGCGCTCTGCCCGCA 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 15172..16569 OTHER INFORMATION: /fu
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                                                                                                                                                                                                                                                                                                                     GTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGGGGCCTTCGGAGCCGTTTACGC 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCGGCCACCGCGACACGGCCGTCCCAGCGCGCGAGCACGGTCTCCAGCTCGTCGCGGG
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                                                                                                                                                                     CGGCCAGCGA
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 THIERRY,
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19149..19398
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16768..17721
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19492..20235
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 Dominique
Veronique
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                                    Jean-Luc
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beta-ketoreductase domain of
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beta-ketoacylACPsynthase doma
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thioesterase domain of module 6"
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; ORIGINAL SOURCE:
; ORGANISM: Myco
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 93/0:
FILING DATE: 13-MAY-1993
PRIOR APPLICATION NUMBER: F 91/1:
APPLICATION NUMBER: F 91/1:
FILING DATE: 31-OCT-1991
ATTORNEY/ACENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
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TITLE OF INVENTION:
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,015
FILING DATE: 02-MAY-1994
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101
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                            CGGTGGACACGGTGATGGTTCCGCCCAG
                                                                            CGCTGGGGCTGCGCAGGCAGAGATCGAAGCCGTGGAGGTGGAGATCGGGCCGCTTCCGAG 1117
                                                                                                                                            ACCAGCAGTACGAGATGCTCAAGCGCTG 1145
                                                           CCCAAGCCGTGCGGTTCGCGCAGGAGGGCGCCGACATCGTGGCCCTCGACCTGTGCGGAC
                                                                                                                       RY: United States
22313-1404
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P.O. Box 1404
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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74
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RESULT 11
US-08-537-002A-4
Sequence 4, Application US/08537002A
Patent No. 5773282
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Best Local
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                   1105
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
                                                                                                           2708 GCGC 2711
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Dianne Casuto
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ADDRESSEE: Abbott Laboratories
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Donadio, S.
Staver, M.J.
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52.7%;
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; MOLECULE TYPE:
US-08-537-002A-4
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SUGIMOTO, TOSHIYUKI
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR
TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE
NUMBER OF SEQUENCES: 17
2668 GAGGCCCTGGAGGCGAGCTTTGGGCCTTTGCCGAGGAGGTGGCCGACCACCTCCACGCC
                                                                                                                                                                                                                                                                                                                                                      2369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                   910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleion STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 260984/1994 FILING DATE: 01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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                                                                                                                                                           GCGCGGCGCTGGAAGGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGCAGAGATCGAAGCC 1089
                                CAGCAGCAGCCCGCGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCCATGGGGCTTGGAC 1209
                                                                                      GTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGTACGAGATGCTCAAGCGCTGGCGC 1149
                                                                                                                                                                                                                                                                              CCCAGCAGAGCTCTTGGCCCCGCTGCTGCCGCCACACTCTCGCCAGAGCTCCCCAGCCGGC
                                                                                                                                                                                                                                                                                                                                                  GCCTTCCCCGCCTCCGGGGGCACGCCCCGGGACCCCAGGCCTCCTTCCCGGGGCCCTGC 2428
                                                                   GTGGAGGAGGACCTGGCCCGGCCTGGCCTACGACGTGGAGCGGGCCGTGCACCTCGCCCTC
                                                                                                                                                                                                                                              TCGCCAGCCATGATGCTGCAGCCGGGCCCGCAGCTCTACGACGTGATGGACGCGGTCCCA 1029
                                                                                                                                     TCCTGGAGCTGG-AGGGGGAGGTGTACCTCGTGGCCCTGGGCGCGCAAAAAGCGGGGCACG
                                                                                                                                                                                                             TTGGGGAGGTGGAGGGGTGGTGGGGGGCCACCCCTCCTAGGCCGCGGCCTCGGGGGCCT
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419 Seventh Street, N.W.,
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KUBOTA, Michio
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46.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                        209;
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1210 GGCTGCGTGGAAGACTTGCGCAGCCGCCTGC

1240

2728 GCCTTCCTCCAAGCCTACCGCTCCGCCCTCC 2758

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; IDENTIFICATION METHOD: US-08-537-002A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application Patent No. 5773282
 Best Local Similarity 46.3
Matches 181; Conservative
                             Query Match
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APPLICANT: TSUSAR
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                              MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                           FEATURE:
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CITY: Washington
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                NAME/KEY: mat peptide LOCATION: 541.3429 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                    ORGANISM: Thermus aquaticus INDIVIDUAL ISOLATE: ATCC 33923
                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP No. 5773282 yet received
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 260984/1994
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LOCATION:
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419 Seventh Street, N.W.,
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SUGIMOTO, TOSHIYUKI
SUGIMOTO, TOSHIYUKI
VENTION: RECOMBINANT THERMOSTABLE ENZYME FOR
VENTION: CONVERTING MALTOSE INTO TREHALOSE
EQUENCES: 17
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Score 44.6; DB pred. No. 0.08; 0; Mismatches 2
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US-07-849-389-6
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Patent No. 5525493
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)833-4109
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HORNES, LATER APPLICANT: UHLEN, Mathias
APPLICANT: UHLEN, MATHIAS
APPLICANT: UHLEN, MATHIAS
APPLICANT: UHLEN, MATHIAS
APPLICANT: HORNES, LATER APPLICANT: HORNES
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920519
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORGANISM:
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1800 Diagonal Road, Suite 500
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Matches
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APPLICANT: Horlick, Robert A.
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Patent No. 5976807
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Best Local Similarity
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT FILING DATE: 1998-08-06
CURRENT FILING DATE: 1998-08-06
RUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
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1204 CTGGACGGCTGCGTGGAAG 1222
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LOCATION:
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nes 129; Conserv
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                                                                TGGCGCCAGCAGCCCGCGGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGG 1203
                                                                                                                                                                     GTGACGGAGGAGCTGGGGCCCGGAGGTGGAGGACGAGGACGGGGAGGACGGGGAGGACGGGGAG
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Pred. No. 0.16;
0; Mismatches 125;
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Patent No. 5876923
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White &
STREET: P.O. Box 4433
2439 CAACCAGAGCCTGCCCCCCCTGCTGGCGGCGGCGGCCAGCGCACCGGACGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                    1074 GCCAGAGATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGAT 1133
                                                                                                                                                                                                                                                                           2199 GCCGCCGCCGCCGACGCGCCCCCCCCCCGCGGGGGGGGCTGCGCGAGCTGCGGTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 160; Conserv
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                                GCGCATGGGGCTGGACGGCTGCGTGGAAGACTTGCGCAGCCGCCTGCAGCGCGGC 1248
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                                                                  GCCGCGGGACCCGCCGCCGAGCTCCGCGGCCGCCGCCGCCGCGGACCTGCTTTGA
                                                                                                  GCTCAAGCGCTGGCGCCAGCAGCCAGCCCGCGGCCCTCGGAGCCGTTTACGCGGCCCTGGA 1193
                                                                                                                                      GGCCGCCGTGGCCCGTGCGCGCGTGAGCCTTGGTCGCCGGGGCCCTGGGCCCCCGCGCT
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Pred. No. 0.19;
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Project (CGAP),

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                                                                                                                                     ALIGNMENTS
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AII40045 xp93y02.x
AII203624 qe75f02.x
AII00459 wd14b11.x
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AII1143 za80h09.s1
AII11528 tw43h06.x
AA476747 zw94b11.r
AA934992 pg31h05.s
AII380959 tg18c01.x
W76376 zd66a06.r1
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AI380900 tg17f01.x
H46374 yo12d07.r1
H46211 yo14h09.r1
AI266746 gq11c06.x
H49675 yo23d06.r1
H41851 yo07f03.r1
H41851 yo12f05.r1
AI913906 wd03f01.x
AA524052 ng33b06.s
AA913870 zd66a06.s1
AA088350 zd86a08.r
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AW182875 xp99a04.x
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N71141 za80g11.s1
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N55389 yz18c11.rl
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A1703436 we24c02.x
AA954505 on81d01.s
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On Apr 7, 1998 this sequence version replaced gi:3035738.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1568 Std Error: 0.00
Seq primer: -40UP from Gibco
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/db_xref="taxon:9606"
/clone="IMAGE:2359204"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
On Jul 7, 1999 this sequence version Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy
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/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/clone="IMAGE:2815679"
                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGGTGCTGCTGGGGGCCCGGGCCCAGGGCGCACTCGTAGCCCCAGGTGTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAGGCATCTCTGAACTAACATACTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGCCTTCTATGAACATGGCGATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTACTGCCAACCATGCCTAGACTGCGGGGGCCCTGCACCGCCACACACGGCTACTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCCTGCCAGGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGGTGCTGCTGGGGGCCCGGGCCCAGGGCGCACTCGTAGCCCCAGGTGTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTAAGCCAGGCTGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACCTTGCTGTGTGTCCCCAAG
                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                     Mammalia; Eutheria; Primates; 1 (bases 1 to 688)
NCI-CGAP http://oww.nci.cgap.nci.com/nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cgap.nci.cga
                                                                                                                                                                                                                                                                                                                                                                                     A1424936 688 bp mRNA EST 30-MAR-1999 tg19b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109207 3' similar to TR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                          2. ;, mRNA
AI424936
                                                                                                                           National Cancer Institute,
                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                     AI424936.1
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95.98;
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Pred. No. 4.1e-123;
D; Mismatches 26;
                                                                                                                                Cancer
                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                  CCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGC
                                                                                                                                                                                                                                                                                                                                   CCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAGGCAGATGTTCTGG
                                                                 GACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCCTGCCCCACGAGCAC 548
                                                                                                                                                                         GGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCCTAGA
                                                                                                                                                                                                                                                                              GCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGT 368
                                                                                                      GCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cence distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2109207"
/clone_lib="NCI_CGAP_CLL1"
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98.3%;
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Pred. No. 4.4e-121;
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ORGANISM
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Best Local :
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                                                                                                                                                                                                                                                                                                          TGGTCTGTTTTGCTTGCAGAGGCTGCCCAGCGGGCACTACCTGAAGGCCCCCTTGCACGGA 188
   GCCCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCCAAGACACCTTCTTGGCCTGGGAGAA 248
                                                                TGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCCTTGCACGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                         561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1640 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 22, 1998 this sequence version replaced gi:3247388 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 494.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
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1 (bases 1 to 562)
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//dev_stage="19 weeks"
//ab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 489.
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AW517358.1
EST.
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1 (bases 1 to 585)
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National Cancer Institute, Cancer Genome Anatomy
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      /organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:2747954"
/clone="IMAGE:2747954"
/clone_lib="Soares_NHCe_cervix"
/lab_host="DH10B (phage_resistant"
/note="organ: cervix; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5' strand cDNA was primed with a Not I - oligo(dT) primer [5' strand cDNA was primed cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."
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                                                    Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
Email: Robert_Strausberg@nih
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 508)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                 AI203624 508 bp mRNA EST 29-OCT-1998 qe75f02.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
Insert Length: 1699
Seq primer: -40UP fr
                        This clone is available royalty-free through LLNL IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                          Tumor Gene Index
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                                                     Robert_Strausberg@nih.gov
  -40UP from Gibco
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                                                                                             CTATGAACATGGCGATGGCTGCGTGTCC 534
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           wt85c09.xl Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2514256 3' similar to TR:014866 O14866 SOLUBLE DE 3 BETA.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      40.5%; Score 508; DB 36; 1 larity 100.0%; Pred. No. 1.8e-104; Conservative 0; Mismatches 0;
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161 c 159 g 106 t
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/lab_host="DH10B (ampicillin_resistant)"
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/db_xref="taxon:9606"
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ATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCCTAGACTGCGGGGGCCCTGCACCG
                                                 ATGTGTCAGGAGTTCACCCCTTCTACTGCCAACCATGCCTAGACTGCGGGGCCCTGCACCG
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                                                                                                                                                              TGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1648 Std Error: 0.00
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Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 410.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
1 (bases 1 to 478)
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Primates;
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Pred. No. 4.4e-90;
0; Mismatches 0;
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       TGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCCTTGCACGGA 180
                                                                                                TGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGGCACTACCTGAAGGCCCCCTTGCACGGA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Oct 30, 1998 this sequence version replaced gi:3812616 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:232803"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                           32.6%;
                                                                                                                                                                                                                                                                                         Score 409.4; DB 4
Pred. No. 2.6e-82;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
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double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was
                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:175727"
                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                       /db_xref="GDB:3837923"
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GGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCCTAGA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 852
High quality sequence stops: 360
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 433)

1 (bases 1 to 433)

1 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H41522 433 bp mRNA EST 31-JUL-1995
yn90f12.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:175727 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
On Dec 20, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 360.
/clone_lib="Soares adult brain N2b5HB55Y"
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                                                                    The WashU-Merck EST Project Unpublished (1995)
On Jun 22, 1998 this sequence version reproduced with the contact: Wilson RK
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                          N71143 432 bp mRNA ES za80h09.sl Soares_fetal_lung_NbHL19W Homo IMAGE:298913 3', mRNA sequence.
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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EST.
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clone
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               est@watson.wustl.edu
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medulla."
129 c 129 g 92 t 3 others
is available
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Pred. No. 9.2e-70;
0; Mismatches 11
royalty-free
through LLNL ;
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                                                                                                                                      AGACTGCGGGGCCCT 440
                                                                                                                                                                             TGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTAC-TGCCAACCATGCC-T
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                                                                                                                                                                                                                                                                                                                                                        TGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGAC-CTACCTGAAGGCCCCCTTGCACGGA 178
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                                                                                                                                                              TGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTTGCCAACCATGCCTT
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                                                                                                                 AGACTGCGGGGCCCT
LILIZE 623 bp mRNA EST tw43h06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone similar to TR:000278 000278 LYMPHOCYTE ASSOCIATE 7. [2] TR:000279 ;, mRNA sequence AI811528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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/db_xref="GDB:1243837"
/db_xref="taxon:9606"
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/dev_stage="19 weeks"
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95.2%;
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Pred. No. 1.1e-64;
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                               ASSOCIATED
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E IMAGE: 2262491
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                    GCCAGCAGCAGCCCGCGGGCCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTGG
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                                                                                                                                                                                                                                                                                                                                     GCTCGCCAGCCATGATGCTGCAGCCGGGGCCCGCAGCTCTACGACGTGATGGACGCGGTCC 1027
                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCCAGGAGAGCTCTTGGCCCCGCTGCTGCTGCCCACACTCTCGCCCAGAGTCCCCAGCCG 967
                                                                                                                                                                                            CCGTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGC
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  ACGGCTGCGTGGAAGACTTGCGCAGCCGCCTGCAGCGCGGCCCGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length. 22.
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2337 Std Error: 0.00
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On Oct 6, 1998 this sequence version
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1 (bases 1 to 623)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.75 kb. Life Technologies catalog # 11538-014"

1 188 c 199 g 128 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IhAGE:2262491"
/clone_lib="NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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96.0%;
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                                                    360 CCCTTCTAGCACCTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACA
                                                                                                                  300 GGATGGAGGCTCTGACCCCACCACCACCACCCATCTGTCACCCTTGGACAGCGCCCACA
                                                                                                                                                   719 GGATGGAGGCTCTGACCCCACCACCGGCCACCCATCTGTCACCCCTTGGACAGCGCCCCACA 778
                                                                                                                                                                                    240 TGACCTACACATACCGCCACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTG
                                                                                                                                                                                                  659 TGACCTACACATACCGCCACTGCTGGCCTCACAAGCCCCTGGTTACTGCAGATGAAGCTG 718
                                                                                                                                                                                                                                                      180
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GCTGGACCCCTGGCTACCCCCGAGACCCAGGAGGCGCTCTGCCCGCAGGTGACATGGTCCT
                                                                   CCCTTCTAGCACCTCCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACA
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                                                                                                                                                                                                                                                                                                                        321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -26ml3 rev2 ET from Amersham
High quality sequence stop: 473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
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zw94b11.rl Soares_total_fetus_nb2HF8_9w
IMAGE.784605 5', mRNA sequence.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Allen, M., Bowles, L., Dubuque, T.,
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/clone="IMAGE:784605"
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/db_xref="GDB:5982223"
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Matches 317; Conserv
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                     GGCTGCCCAGCGGGGCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACC 207
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GGCTGCCCAGCGGGCAGCTACCTGAAGGACCCTTGCACGGAGCCCTGCGACAACTCCACC
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1648 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 131.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Apr 21, 1998 this sequence version replaced gi:3072128 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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op33h05.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:15786813' similar to TR:014866 014866 SCLUBLE D
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1578681"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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943 ACACTETEGECAGAGTECCCAGCEGGCTCGCCAGCCATGATGCTGCAGCCGGGCCCGCAG 1002

Query Match Best Local S Matches 295

Local Similarity

295;

Conservative

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Score 284.8; DB 3 Pred. No. 2.8e-54; 0; Mismatches 17

Indels Length 587;

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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1380959 587 bp mRNA EST 30-MAR-1999 tg18c01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109120 3' similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. ConsortLum/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1237 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Oct 8, 1998 this sequence version replaced gi:3730839
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert_Strausberg@nih.gov
                         a
                                                                                                                                adaptors (Pharmacia), digested with Not I the Not I and Eco RI sites of the modified Library is normalized, and was constructed Soares and M.Fatima Bonaldo."

192 c 176 g 120 t
                                                                                                                                                                                                                                               /clone="IMAGE:2109120"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"_____
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                              double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
                                                               the modified pT7T3 vector.
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FEATURES
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 969 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Med: 4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
On Jan 7, 1998 thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 372)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W76376 372 bp mRNA EST zd66a06.rl Soares_fetal_heart_NbHH19W Homo IMAGE:345586 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                       primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                   quality sequence stop: 352
Location/Qualifiers
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                       /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:345586"
/clone="IMAGE:345586"
/clone=lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998 this sequence version
                                                                                                                                                                                        /sex="unknown"
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GCACCGTCCAGTTGGGTGGGTAACAGCTGGACCCCTGGCTACCCCCGAGACCCCAGGAGGCGC
                                                                                                                                                                                                                   TGTCACCCTTGGACAGCGCCCACACCCTTCTAGCACCTCCTGACAGCAGTGAGAAGATCT 814
                                                                          TCTG-CCGCANGTGACATGGTCCTGGGA-CAGTTGCCCAGCAGA-NTCTTGGCCCCGCTG
                                                                                                               TCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGCCCCAGCAGAGCTCTTGGCCCCGCTG
                                                                                                                                                     GCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTGGCTACCCCGAGACCCCAGGAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                  normalization to a Cot = 5. Library constructed by M.Fatina Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

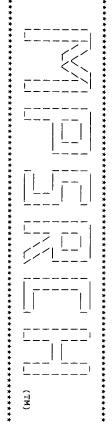
a 133 c 106 g 59 t 3 others
                                                                                                                                                                                                                                                                                                                    21.8%;
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                    Score 273.2; DB 9 Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                                                                                                 91;
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Search Job tim time: completed: July ne: 4247 sec 23, 2000, 06:13:02

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:22:14 2000; MasPar time 13.99 Seconds 724.413 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US-09-314-889-2 (1-428) from US09314889.pep 3267 1 MEETQQGEAPRGQLRGESAA.....ERMGLDGCVEDLRSRLQRGP 428

Scoring table: PAM 150 Gap 11

188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 35.731; Variance 153.828; scale 0.232

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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387 372	400 394	400 400	404	407	407	407	408	412	503	1342	1962	3118	3118	3118	3118	3118	3267	3267	Score
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R51032 R24000	R42197 R12550	R51033 R51034	R11082 R20787	R42059	R75084	R10986	R07451	W64485	W93610	W26708	W57046	W64486	W57045	W95538	W26709	W31517	W95537	W31516	ID
p55 pha 5		Mutant p55 tumour necr	Human 55kD TNF-binding TNF-alpha binding prot	Lambda derived TNF-R.	p55 TNF-R.	∺	Tume	Fas protein	DR3 prote	apoptosis	Mouse apoptosis induci	Human DR3 protein.			Human apoptosis protei		Death domain containin	Death domain containin	Description
	2.29e-25 8.27e-25	2.29e-25 2.29e-25	9.71e-26 9.71e-26	5.10e-26	5.10e-26	5.10e-26	4 126-26	1 746-26	4.88e-35	1.40e-116	6.35e-178	4.51e-293	4.51e-293	4.51e-293	4.51e-293	4.51e-293	0.00e+00	0.00e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
240	243	246	246	246	246	246	246	246	246	246	246	246	246	246	245	246	246	245	248	271	351
7.3	7.4	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.6	8.3	10.7
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R27496	R70109	R70105	R70106	R70103	R70104	R70107	W89224	W89226	W89227	R07449	W89228	W89229	R70108	W33358	W33359	W89225	R24080	W73570	W33360	W33357	R07450
Native 30 kD TNF inhib	TNF-R-GBP 130 fusion p	TNF-R-EBA 175 fusion p	TNF-R-Pl. vivax Duffy	TNF-R-GBP 130 fusion p	TNF-R-GBPH fusion prot	TNF-R-GBP 130 fusion p	Tumour necrosis factor	TNF-R-GBPH fusion prot	TBP(20-161)/hCG-beta f	TBP(20-190)/hCG-alpha	Tumour necrosis factor	Truncated TNF-alpha 55	Cytoplasmic domain of	TBP(20-190)/hCG-beta f	TBP(20-161)/hCG-alpha	Rat Tumour Necrosis Fa					
8.03e-11	4.37e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.38e-11	2.91e-11	2.38e-11	2.38e-11	2.91e-11	1.58e-11	1.43e-13	7.82e-21

## ALIGNMENTS

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Best Local Similarity 100.0%;
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                                        06-JAN-1999.
12-MAR-1997; 057503.
06-FEB-1997; US-037341.
12-MAR-1996; US-013285.
17-OCT-1996; US-028711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This protein comprises human death domain containing receptor DR3-VI, a novel member of the tumour necrosis factor receptor family. Its amino acid sequence was deduced from a cDNA clone (see T89426) isolated from a human testis tumour library. Related death domain containing receptor DR3 (see W31517) has also been identified. Recombinant full-length or mature DR3-VI can be expressed in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the inhibition of apoptosis, or to screen for modulator compounds. Antagonists, such as antibodies raised against DR3-VI, can be used to treat diseases and disorders associated with increased apoptosis and for treating inflammatory diseases and disorders.
                                                                                                                                                                                                                                                 W95537 standard; Protein; 428 W95537;
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               (HUMA-)
  WPI;
                                                                                                              J11000170-A.
                                                                                                                                         Protein
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                                                                                                                                                                                            Homo sapiens.
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UNIV MICHIGAN.
1-124390/11.
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                                                                                                                        /note= "signal peptide"
36. .428
/note= "mature protein"
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                        preceptor DR3-V1; D
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Pred. No. 0.00e+00;
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W09733904-A1.
18-SEP-1997.
17-OCT-1996; U
                                                                                                                                                                                                                                                                                                                                                                            Death domain containing Death domain containing inflammation; NF-kappaB
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428; Conservative
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e= "transmembrane
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Chaim 1; Page 75-77; 108pp; English.

This protein comprises human death domain containing receptor DR3, a novel member of the tumour necrosis factor receptor family. Its amino acid sequence was deduced from a DNA clone (see T89427) isolated from a HUVEC cDNA library. Related death domain containing receptor DR3-V1 (see W31516) has also been domain containing receptor DR3-V1 (see W31516) has also been domain containing receptor DR3-V1 (see W31516) has also been domain containing receptor DR3-V1 (see W31516) has also been domain containing receptor DR3-V1 (see W31516) has also been domain containing receptor DR3-V1 (see W31516) has also been domain of identified. Recombinant full-length or mature DR3, or the extracellular or death domain of DR3 can be expressed in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the CC inhibition of apoptosis, or to screen for modulator compounds. CC antagonists, such as antibodies raised against DR3-V1, can be used to treat diseases and disorders associated with increased apoptosis and for treating inflammatory diseases and disorders.
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(UNMI ) UNIV MICHIGAN.
Dillon PJ, Dixit VM, Gentz
                                                                                                                                                                                                                                                                                                                W26709 standard;
W26709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Death domain containing receptor polypeptide(s) DR3 and DR3-V1 for activation of apoptosis and NF kappaB, antagonists can be to treat inflammatory diseases Claim 1; Page 75-77; 108pp: English
                                                                                                         Domain
                                                                                                                                                    Peptide
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                          Human apoptosis protein
                                                                                                                                                                                                                                     Apo-3;
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No. 4.51e-293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This movel polypeptide, designated Apo-3, is a protein that stimulates or induces apoptotic activity in mammalian cells purposes. Its amino acid sequence was deduced from a human foetal cheart CDNA clone (see T91180). The N-terminal 181 amino acids of Apo-3 are identical to the sequence of another novel apoptosis polypeptide, Apo-2II (see W26709). Also claimed are: polypeptides comprising the extracellular or death domain of Apo-3; chimeric molecules comprising Apo-3 fused to a heterologous amino acid sequence; antibodies that bind to Apo-3 or its extracellular domain; nucleic acids encoding the polypeptides, as well as vectors and host cells; a non-human transgenic animal containing cells that express nucleic acid encoding Apo-3; and a non-human cells that animal containing cells having an altered Apo-3 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in mammalian cells
Claim 19; Page 46-48; 70pp;
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                       VEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                              PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
                                                                                                                                                                                                                               LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
                                                                                                                                                                                                                                                                                                PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
VEVEIGRERDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                    LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
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US-710802.
US-625328.
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designated Apo-3,
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Pred. No. 4.51e-293;
3; Mismatches 4;
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12-MAR-1997; US-037341.
06-FEB-1997; US-037341.
12-MAR-1996; US-013285.
17-OCT-1996; US-028711.
(HUMA-) HUMAN GENOME SCI INC.
M57045 standard; |
W57045;
W57045;
20-AUG-1998 (fir:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents the amino acid sequence of a death domain containing receptor
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                                                                                                                                                                                               VEVEIGRERDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                               PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                     LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTST 183
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                                                                                                                                                                                                                                                                                        PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
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417 AA;
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25. .417
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                                                        Protein; 417
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98.3%;
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No. 4.51e-293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding apoptosis inducing receptor - which is Type I transmembrane protein, useful for regulating cell death (Claim 16; Page 28-30; 45pp; English.

This sequence is the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases. Sequence 417 AA;
30-JUL-1998.
27-JAN-1998;
05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human apoptosis inducing receptor.

Apoptosis inducing receptor; AIR protein;

Transmembrane protein; tumour cell
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03-OCT-1997; U17876.
04-OCT-1996; US-044456.
                                                                                    Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation; agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; DR3;
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N-PSDB; V28700
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                                                                                                                   Human DR3
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                                                        Homo sapiens.
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                                            WO9832856-A1.
                                                                        nfection; graft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE 63
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                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%;
Similarity 98.3%;
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U01464.
US-037829
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Pred. No. 4.51e-293;
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                                                                           inhibitor;
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                                                                           diagnostic
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disease;
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                                                                                                                                Type
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                       09-APR-1998.
03-OCT-1997; U17876.
04-OCT-1996; US-044456.
(IMOV) IMMUNEX CORP.
                                                                                    Mus sp.
W09814565-A1.
                                                                                                                                             Mouse apoptosis inducing receptor.

Apoptosis inducing receptor; AIR protein;
                                                                                                                                                                                                       W57046 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for therapeutic autoimmune diseases
               Perkins
                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR3 which is used in a method resulting in the isolation of a human death domain containing receptor 4, DR4. DR4 agonists are used to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to detect mutant forms isolating the DR4 gene Sequence 833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human death
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Dixit VM, Gentz RL, Ni
                                                                                                                                                                           20-AUG-1998 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding human death
                                                                                                                                                                                                                                                                   375
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                                                                                                                                                                                                                                                                                                                                                                                                                                            98-240077/21
                                                                                                                               I transmembrane
                                                                                                                                                                                                                                                                VEVEIGRERDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98-427952/36
                                                                                                                                                                                                                                                                                             VEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                        PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
                                                                                                                                                                                                                                                                                                                                                                                                 LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                   LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGESAAPVPQALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL, Ni J, Pan
                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.4%;
98.3%;
                                                                                                                                                                           entry)
                                                                                                                               protein; tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 3118; DB 1;
Pred. No. 4.51e-293;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of apoptosis,
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                                                                                                                               ; mouse;
l death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing receptor-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                               cell death regulator;
autoimmune disease;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AII can also be used in vitro to block apoptosis or AIR-expressing cells, out to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting a well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases Sequence 411 AA;
                                                                                                                                                   31-MAR-1997; U05230.
23-SEP-1996; US-710802
01-APR-1996; US-625328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein, useful for regulating cell
Claim 16; Page 33-35; 45pp; English.
This sequence is the mouse apoptosis inducing receivemention. AIR is a Type I transmembrane protein,
Polypeptide(s) Apo-3 in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human apoptosis protein Apo-2LI. Apo-2LI; apoptosis; Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W26708;
14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 9
W26708 standard;
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DNA encoding apoptosis inducing receptor - w.
                                                  N-PSDB; T91179.
                                                                                                     Ashkenazi AJ;
                                                                                                                                                                                                                                                         WO9737020-A1
                                                                                                                                                                                                                                                                                                               Modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                           (GETH ) GENENTECH
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                                                                             97-503105/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQQYEMLKRWRQQQPAGLGAIYAALERMGLEGCAEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLLLGGQGQGGM-SGRCDCASESQKRYGPFCCRGCPKGHYMKAPCAEPCGNSTCLPCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASPLSPAPPAGSPAAVLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEICRFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLDSAHTLLAPPDSSEKICT-VQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASDSAHTLLAPPSSTGKICTTVQLVGNNWTPGLSQTQEVVCGQASQPWDQLPNRTLGTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCW-PHKPLVTADEAGMEALTPPPATHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGWKQMFWVQVLL-G--VAFLFGAILICAYCR-WQPCKAVVTADTAGTETLASPQTAHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFSCVPCGATTPVH-EAP---TPR----PCLPGFYIRGNDCTSCPTGFSSVCPKACTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDTFLTRDNHFKTDCTRCQVCDEEALQVTLENCSAKSDTHCGCQSGWCVDCSTEPCGKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267;
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                                                                                                                                                                                                                                                                                                                                                               /label=
67
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                            /note= "N-glycosylated"
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.1%;
65.9%;
                          and
                                                                                                                                                                                                                                                                                 "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                    Sig_peptide
                        Apo-2LI
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Pred. No. 6.35e-178;
61; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor;
                          useful
                     for regulating apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 16;
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Soluble AIR
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                                Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                               extracellular receptor, transmembrane and death domains. The nuclear discount which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful diagnosis and treatment of neoplastic diseases. The invention is useful for the production of animal model systems.

Sequence 65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibit mammalian cell apoptosis in vivo or ex vivo, and in quantitative diagnostic assays.

Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This novel (Apo-2LI),
                                                                                                                                                                                                                                                                                                                                              04-AUG-1997; US-054710.
30-SEP-1997; US-060473.
11-MAR-1998; US-077526.
11-MAR-1998; US-077628.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and cytoplasmic sequences of Apo-3. Apo-2LI can be produced in host cells using a claimed method. Chimerle polypeptides comprising Apo-2LI fused to a heterologous amino acid sequence, and an Apo-2LI dimer are also claimed. Apo-2LI can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA clone (see T91179) and is identical to amino acid residues 1-181 of another novel apoptosis polypeptide, Apo-3 (see W26709). It may be a soluble, truncated of secreted form of Apo-3, lacking some extracellular sequence as well as the transmembrane
                                                                                                                                                                              apoptosis mediating activity and comprises an amino-terminal extracellular receptor, transmembrane and death domains. The
                                                                                                                                                                                                                               Disclosure; Page 46; 65pp; English.
This invention describes a novel human adriamycin-inducible killer
                                                                                                                                                                                                                                                            induces apoptosis and neoplastic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis; p53-inducible; apoptosis-mediating activity; treatment; animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 10
W93610 standard; Protein;
                                                                                                                                                                                                                protein located on chromosome 8p21, which also has p53-inducible,
                                                                                                                                                                                                                                                                                                                                  El-Deiry WS,
                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1998; U14495.
11-MAR-1998; US-077661.
11-JUL-1997; US-052305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9902653-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DR3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W93610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PI; 99-120857/10.
new nucleic acid encodes a p53-induced protein (Killer) - whinduces apoptosis and is useful in the diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 134
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 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGESAAPVPQALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
171; Conser
                             15.4%;
Similarity 100.0%;
65; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 43-44; 70pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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No. 1.40e-116;
                                               503; DB 1;
No. 4.88e-35
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Best Local Similarity 30.1%;
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27-JAN-1998, U01464.
27-JAN-1997; US-037829.
28-JAN-1997; US-035722.
(HUMA-) HUMAN GENOME SCI INC.
(UNMI) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resulting in the isolation of a human death domain containing receptor 4, DR4 agonists are used to increase apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of cancer, autoimmune disease, viral or other infections, inflammation, graft vs. host disease, acute or chronic graft rejection. Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune deficiency syndrome, neurodegenerative disease, myelodysplastic syndrome, ischaemic injury, toxin-induced liver damage, septic shock, cachexia and anorexia, also a wide range of inflammatory conditions. DR4 of fragments of the protein are used diagnostically, e.g. to detect mutant forms of DR4 (possibly associated with disease), for isolating the DR4 gene or related sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation; agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; infection; graft rejection; antagonist; inhibitor; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases
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Nucleic acid encoding human death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W64485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9832856-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                          26 VIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGP-GDTDCRECES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for chromosomal mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ 86
                                                                                                          GELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP
                                                                                                                                                                                 QIENVKGTEDSGTTVLLP-LVIFFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKE
                                                                                                                                                                                                                                                         FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP 195
                                                                                                                                                                                                                                                                                                                                 GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC- 141
 -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                      PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
                                                                      A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
                                                                                                                                                                                                                       FYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG-SCPERC-A
                                                                                                                                                                                                                                                                                             DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    909 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 412; DB 1;
Pred. No. 1.74e-26;
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raTNF-R8 (Q06284) was used to screen the HS913T cDNA library. LambdaTNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same as pADTNF-BP (see Q06282). The expressed proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1991 (first entry)
Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.
Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
infectious disease; parasitic disease; cachexia;
autoimmune disease; shock; lambdaTNF-R2; raTNF-R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        respiratory distress syndrome etc., or side effects of treatment with TNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions. See also Q06282-Q06285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prophylactically and therapeutically to control disorders which involve the damaging effects of TNF-alpha or -beta (e.g. infectious parasitic diseases, shock, cachexia, autoimmune diseases, adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q06285
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21-JUN-1989;
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21-JUN-1989; DE-920282.
(BOEH ) BOEHRINGER INGELHEIMINT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECES
RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                             PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
                                                                                                                                                                     A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                              GELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP
                                                                                                                                                                                                                                                                                      AVCGWROMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
                                                                                                                                                                                                                                                                                                                       LIGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
                                                        -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                 FYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG-SCPERC-A
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No. 4.12e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of TNF inhibitor for use in the treatment to claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and beta, useful as therapeutic agent.

Disclosure; Fig 21; 142pp; English.

The sequence comprises the entire 30 kD TNF inhibitor. The clone from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA. The whole gene can be inserted into expression vectors for prepn. of TNF inhibitor for use in the treatment of inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour
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07-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q10883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYNE-) SYNERGEN INC WPI; 91-073847/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30kD TNF inhibitor precursor. Tumour necrosis factor; inhib
437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1990;
18-JUL-1989;
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IEEAL
                                                 TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP--
                                                                                                                                                                             PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
                                                                                                                                                                                                                                                                                                GELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP
                                                                                                                                                                                                                                                                                                                                                                                FNCSLCLN-GTVH-----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                                                                                                                                                              A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                                                 AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
                                                                                                                                              -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG-SCPERC-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC-
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127; Conser
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441
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US-450329.
US-479661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
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Pred. No. 5.10e-26;
81; Mismatches 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - for suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            active

    AGLGAVYAALERMGLDGCVED

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δÃ

420 LRSRL

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RESULT ACCORDED TO THE RESULT OF THE PROPERTY 
Matches
                                          Best Local
                                                                      Query Match
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R75084;
19-JAN-1996 (fir
                                                                                                                                                                                                                        spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidernal growth factor receptor (EGF-R) that are represented by R75007-11. This spacer region was subjected to deletion mutations (R75013-25) and substitutions (R75026-47). Of the spacer region, the most important residues are Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most important of these. The shedding of the receptor is independent of the side chain identity of these residues, with the exception of a limited dependence on the identity of Val 173. Mutations which alter the conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an inhibitor of a protease that is capable of cleaving the soluble TNF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 40pp; English.

This sequence represents human p55 tumour necrosis factor (TNF-R).

Expression of this receptor is regulated by shedding of the extracellular receptor fragment. The p55 TNF-R can be shed in response to different inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell type. The only region of the receptor whose structure affects the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L2-OCT-1993; IL-107268.

(YEDA ) YEDA RES & DEV CO
Batkin M. Brakebusch C,
WPI; 95-194342/26.

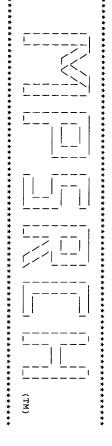
N-DCDD - 07677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shedding response is the spacer region (see R75012) in the extracellular domain. This region is located close to a site of cleavage of the molecule, and links the Cys rich module to the transmembrane domain. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
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                                                                                                                                                                              from the cell bound TNF-R. Fragments of these inhibitors can R75017-9, R75025, R75033-5 and R75042-3. These protease inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonising deleterious Disclosure; Fig 1; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protease capable of cleaving soluble tumour necrosis (TNF) receptor - from cell-bound TNF- receptor, useful i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-1994; 075742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour necrosis factor receptor; TNF-R; human; murine; chimera;
ermal growth factor receptor; EGF-R; protease; inhibitor;
                l Similarity
127; Conser
                                                                                                                                                     for
                12.5%;
llarity 29.9%;
Conservative
                                                                                                                                                  enhancing
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                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
201
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161. .163
/note= "g]
193. .210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "major C terminus for soluble p55 TNF-R" 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
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198. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145.
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Pred. No. 5.10e-26;
81; Mismatches 177;
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                                                                                                                                                                                                                                                                              14-OCT-1993.
26-MAR-1993;
30-MAR-1992;
                                                                                                                          New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral mala
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R42059;
29-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R42059 standard; Protein; 455
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                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lambda derived TNF-R
                                               TNF-R-linker-TNF-R-linker-IL-1R
                                                                                                                                                                                                                 N-PSDB; Q49932.
                                                                                                                                                                                                                                                Smith CA;
TNF-R-linker-TNF-R
                                                                              factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-1R). These sequences were used the production of a fusion protein which conformed to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                               Lambda-gt10-7ctnfbp
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                                [L-1R-linker-TNF-R-linker-TNF-R
                                                                  formulae:
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune dysfunctions. Sequence 455 AA;
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Local Similarity 29.9%;
les 127; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:21:31 2000; MasPar time 23.74 Seconds  $850.475\ \mbox{Million}$  cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-314-889-2 (1-428) from US09314889.pep 3267

Sequence: 1 MEETQQGEAPRGQLRGESAA.....ERMGLDGCVEDLRSRLQRGP 428

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.837; Variance 92.768; scale 0.516

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

21 22 23	16 17 18 19 20	13 14 15	. 6 . 7 . 8 9 10	να 4 τυ <i>γ</i>	Result No.
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heparan sulfate prote	laminin beta-1 chain	glutamyl-tRNA synthet	A53R protein - vaccin	laminin gamma-1 chain	laminin gamma-1 chain	integrin beta-5 chain	CD40 - mouse	B cell-associated sur	nidogen precursor – h	OX40 homolog - human	integrin beta-5 chain	hypothetical protein	MEGF6 protein - rat	laminin alpha 5 chain	hypothetical protein	Fas-Delta-(4,7) prote	Fas/Apo-1/CD95 protei	nerve growth factor r	serine/threonine prot	receptor interacting	nerve growth factor r
1.13e-01	1.13e-01	1.13e-01	1.53e-01	4.49e-02	6.11e-02	6.11e-02	8.31e-02	8.31e-02	2.40e-02	2.40e-02	1.28e-02	9.32e-03	2.57e-03	9.65e-04	9.65e-04	6.94e-04	6.94e-04	9.31e-05	3.35e-05	3.35e-05	5.94e-06

## ALIGNMENTS

ession A34900	#accession
tumor necrosis factor. cross-references MUID:90235285	#cross-refe
Molecular cloning and expression of a receptor for human	#title
H.; Kohr, W.J.; Goeddel, D.V. Cell (1990) 61:361-370	#journal
Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,	
Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;	#authors
A34900	REFERENCE
part of this sequence, including the amino end of the	##note
<pre>#experimental_source placenta</pre>	##experi
PID: 9339754	
ferences GB:M58286;	##CIOSS-
2S 1-455 ##label LOE	##residues
##molecule type mRNA	##molecu
A34899	#accession
necrosis factor receptor.	= 01000
Molecular cloning and expression of the human 55 kd tumor	#title
Cell (1990) 61:351-359	#journal
000000	
Loetscher H . Dan V C E . Lahm H W . Centz R . Brockhaus	#authors
A34899	REFERENCE
#cross-references GB:M/5864; GB:M/5865; GB:M/5866; NID:g339748; PIDN:AAA61201.1; PID:g339750	##Cross-
1-455 ##Label	##residues
_type DNA	##molecu
A38208	#accession
#cross-references MUID:92250049	#cross-refe
chromosome 12p13.	
Structure of the human TNF receptor 1 (p60) gene (TNRF1) and	#title
	# journal
Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.	#authors
JTU/38; A0UZ31; A38Z38; A6U394; A33U1U; JCZ4U4 A38208	REFERENCE
A38208; A34899; A34900; A36555; C36555; A38281; S12057;	ACCESSIONS
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change	DATE
binding protein 1 (TNF blocking factor)	ORGANISM
	CONTAINS
tumor necrosis factor receptor l precursor - human PPS tumor necrosis factor receptor: TNF receptor	TITLE ALTERNATE_NAMES
GQHUT1 #type complete	ENTRY
	RESULT 1

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##cross-references GB:M33294;
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##cross-references GB:M63121; NID
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##cross-references GB.M37764
the authors translated the codon TGG for residue 371 as
##note Thr, AAG for residue 372 as Leu, and GAC for residue
                                  ##molecule_type protein
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Kemper, O.; Wallach, D.
Gene (1993) 134:209-216
Cloning and partial characterization of the promoter for human p55 tumor necrosis factor (TNF) receptor.
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R.; Aderka, D.; Holtmann, H.; Wallach, D.
EMBO J. (1990) 9:3269-3278
Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
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Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protei
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                                                                                         Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
                                                           A60231
                                                                                                                                                              Eur. J. Immunol. (1990) 20:1167-1174
                                                                                                                                                                                                  Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield,
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107-128;162-167,'X',169-201 ##label HI2
the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the
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#title Isolation and characterization of a binding protein from urine. #cross-references MUID:89171156
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#introns
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#accession JC2404
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ap_position 12p13.2-12p13.2

atrons 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
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2NCE A60594
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WT This protein is one of two known receptors for both TNF-alpha
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##residues 41-53,'x',55-144,'x',146-150,'x',152-186,'x',188-201
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##residues 41-45 #
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##residues 41-60 #
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##residues 41-43,'X',45-53,'V',55-57,'XK',60
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Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily tumor necrosis factor receptor type 1;
receptor repeat homology
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#length 455
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                                                                                                                                  #domain extracellular #status predicted #label EXT\
#product TNF binding protein 1 (tumor necrosis facto)
alpha inhibitor) #status experimental #label TBP1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
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#product tumor necrosis factor receptor type 1 #statu
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Best Local Similarity 29.9%;
Matches 127; Conservative
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                                                                                                                                                                                  murine receptors for tumor reces MUID:91246168
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##cross-references GB:M60468;
                                                                                                                                            ##molecule_type mRNA
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                                                                                                                                                                                                       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T
C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.
Mol. Cell. Biol. (1991) 11:3020-3026
Molecular cloning and expression of the type 1 a
murine receptors for tumor necrosis factor.
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tumor necrosis factor receptor 1 precursor - mouse
tumor necrosis factor receptor, 55K
#formal_name Mus musculus #common_name house mouse
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
Eur. J. Immunol. (1991) 21:1649-1656
Cloning, expression and cross-linking analysis of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis, M.: Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834 Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.
                                                                                    S16677
                                                                                                                                                                   B40254
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Pred. No. 4.79e-55;
                                                                                             GO2
NID:g199825;
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                                                                                                   PIDN:AAA39751.1; PID:g199826
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COMMENT This protein is one of two Accessions.
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127-167
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#accession I54532
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#accession S19021
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##cross-references EMBL:X57796; NID:g54848;
                   332 SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                                 264
                                                                                                                                                                                           215
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                                                                                                                                                                                                                                                                                                                                                           98 QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP 157
                                                                                                                                                                                                                                                                                                                                                                                                      40 RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                              40 RDSLCP-QGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                WRQMFWVQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                                        SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                                                                                                                                                   CGALHRHTRLLC-SR---RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG
                                                                                                                                                                                                                                                                          CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
                                                                                                        SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                                                                                                                                                                                                                                   ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQPCLD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein is one of two distantly related receptors TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 12.2%;
Similarity 28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily tumor necrosis factor receptor type 1; NGF
   receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenetics (1994) 39:450-451 Nucleotide sequence of the TNF t endothelioma cell line.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bebo, B.F.
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#domain NGF receptor repeat homology #label NG4\
#domain NGF receptor repeat homology #label NG4\
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Pred. No. 1.86e-53;
79; Mismatches 182
Mismatches 182; Indels 34;
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for both
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84-126
211-231
361-447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
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##cross-references GB:U19994; NID:gl141752;
PID:gl141753
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   255
                                                                      210
                                                                                                                                                                               144
                                   261 LATAPSFGPITTFSPIPSFSPTTTFSPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPP 320
                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #molecule_type protein
1-7 ##label SU2
                                                                                                                                                                                                                   93
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                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                       33 HPGDREKRESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTAS 92
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                              LNC-SLCPNGTVQLPCLEKQDTICN-CHSGFFLRDKECVSCVNCKNADCKNLCPATSETR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGR-FRDQQYEMLKRWRQQQP--AG-LGAVYAALERMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                                    ENHL-TQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKN---QYR--KY-WSETLF-Q-C 143
                                                                                                                                                                                                                                                                                   QGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAW 92
                                                                                                       NDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQR-WKPKLYSIICGKSTPVKEGEPEP
                                                                                                                                                                                                                 ENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC 152
                                                                                                                                            LDCGALHRH-T-RLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWR
                                                                                                                                                                                                                                                                                                                                                              139;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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tumor necrosis factor receptor p55 precursor - pig
#formal_name Sus scrofa domestica #common_name domestic
29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suter, B.; Pauli, U.
Gene (1995) 133:263-266
Cloning of the cDNA encoding the
factor receptor.
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glycoprotein; kidney; receptor; transmembrane protein;
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JC4302
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                                                                                                                                                                                                                                                                                                                                                                                                                              #length 461 #molecular-weight 50696 #checksum 8079
   -PATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTP---GYPETQEALCP
                                                                                                                                                                                                                                                                                                                                                              Conservative
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#domain NGF receptor repeat homology #label NGF\
#domain transmembrane #status predicted #label TMM\
#domain signal transduction #status predicted #label
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Pred. No. 2.93e-53;
81; Mismatches 160
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##cross-references GB:M76656;
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                                                                                                                                                                                                                                                                                                                                                                                                             RDSLCP-QGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-
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                                                                                                                                                                                                                                                                                                                                              QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP 157
                                                                                                                                                                                                                                                                                                                                                                               RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS 98
 PAAAPTLSPESPAGS-PAMMLQPG-PQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVE
                                                                                           SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                                                                                                                                                          WROMFWVQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                                                                                      LPLVILLGLCLLSFIFISLMCRYPRWRPEVYSIICRDPVP-VKEEKAGK-PLTPAPSPAF 272
                                                                                                                                                                                                                                                     CGALHRHTRLLC-SR----RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG
                                                                                                                                                                                                                                                                                  CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
                                                                                                                                                                                                                                                                                                                   ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC -- QVS-QCVSSSP-FYCQPCLD 154
                               NGGCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENILEAL-RNP 444
                                                                                                                          SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                                                                         SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                                                                                                                                                                                                                                                                                                                                                            118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%;
Similarity 28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; #superfamily tumor necrosis factor receptor type 1; NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Immunol. (1993) 30:165-176
Genomic organization and promoter function
tumor necrosis factor receptor beta gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain NGF receptor repeat homology #label
#length 454 #molecular-weight 50030 #checksum o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 385; DB 2;
Pred. No. 1.09e-50;
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NID:g202100; PIDN:AAA40465.1;
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84-126
127-167
168-204
212-234
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30-201
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    314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-461 ##label HIM
##cross-references GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
## This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxi).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 GDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQN 94
                                                                                                                                                                                                                                 LLPLVIFLGLCLLFFICISLLCRYPQWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASI 272
LPSRALGPAAAPT-LSP-ESPAGSPAMMLQPG-PQ-LYDVMDAVPARRWKEFVRTLGLRE
                                           LLYGSLNPVPIPAPVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSE 389
                                                                                                                                     PAFSPNPGFNPTLGFSTTPRFSHPVSSTPISPVFGPSNWHNFVPPVREVVPTO-G-A-DP 329
                                                                                                                                                                                      GWRQMFWVQV-LLAGLVVPLL--LGATLTYTYRH-CWPHKPLVTADEAGM--EALTPPPA
                                                                                                                                                                                                                                                                                PCLDCGALHRHTRLLCSRRDTDCGT-CLP-GFYEHGDGCVS-C-PTSTLGSCPERCAAVC 206
                                                                                                                                                                                                                                                                                                                           VTIPCKE-KONTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAV 212
                                                                                                                                                                                                                                                                                                                                                                          HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                     H-VRQCLSCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTRSPRCD-CA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN 94
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Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.
Stratowa, C.; Adolf, G.R.
DNA Cell Biol. (1990) 9:705-715
Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length
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tumor necrosis factor binding protein 1 (TWF blocking factor)
#formal_name Rattus norvegicus #common_name Norway rat
30_Jun-1992 #sequence_revision 07-Oct-1994 #text_change
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#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label INT\
#domain intracellular #status predicted #label INT\
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#product tumor necrosis factor binding protein #sta
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73; N
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Pred. No. 2.72e-50;
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Olsson, I.; Hauptmann, R.;
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#cross-references MUID:92148151
#accession A46484
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##experimental_source liver
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:cession PC2246
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                                                                                                                                                                                                                                                                                                                                                                                               CQACDE-QASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC-LDCGALHR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCAGDFHKKIGLFCCRGCPAG-HYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECAR
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Similarity 30.1%;
37; Conservation
                                                Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, Copeland, N.G.; Jenkins, N.A.; Nagata, S. J. Immunol. (1992) 148:1274-1279
The cDNA structure, expression, and chromoso
                                                                                                                                                                              #formal_name
18-Jun-1993 #
                                                                                                                                                                                                                            A46484 #type complete apoptosis-mediating membra
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JC2395
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20-Feb-1995 #sequence_revision
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                                   the mouse Fas antigen
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antigen precursor - rat
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#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label TMM
#domain transmembrane #status predicted #label TMM
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                                                                                                                                                                            #sequence_revision
                                                                                                                                                                              Mus musculus #common_name hou
#sequence_revision 18-Nov-1994
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                                                                                                                                                                                                                                membrane-associated polypeptide
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Commun. (1994) 198:666-674
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20-Feb-1995
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112 QVALENCSAVADTRCGCKPGWFVECQVS-QC

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81-124
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
#title Aberrant transcription caused by the insertion of an early
transposable element in an intron of the Fas antigen gene
of lpr mice.
#cross-references_MUID:93189576
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#cross-references MUID:95181785
#accession 137383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-327 ##label WAT ##cross-references GB:M83649; NID:g193225; PID:g193226 ##experimental_source BAM3 macrophage cell line
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                                                                                             56 GQFCHKPCPPGE-RKARDCTVNGDEPDCVPCQEGKEYTD-KAHFSSKCRRCRLCDEGHGL 113
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                  EVEI-NCTRTQNTKCRCKPNFFCNSTVCEHC
                                                          GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 111
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NCBIN:126853, NCBIN:126863, NCBIP:126864)
#superfamily NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                   Cascino, I.; Fiucci, G.; Papoff, G.; Rubert:
J. Immunol. (1995) 154:2706-2713
Three functional soluble forms of the human
apoptosis-inducing Fas molecule are produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137383 #type complete
FAS soluble protein human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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larity 27.9%;
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#length 327
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#domain NGF receptor repeat homology #label
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34.1%;
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Pred. No. 1.26e-16;
19; Mismatches 52;
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                                                                                                                                                        Score 190; DB 2;
Pred. No. 3.26e-14;
                                                                                                                                      Mismatches
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#accession A40036
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ap_position 10q24.1-10q24.1
IFICATION #superfamily NGF receptor repeat homology
   112
                                     114
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##status preliminary; not compared ##mollecule_type nucleic acid acid ##residues 1-134,'0','136-335 ##label ##experimental_source SKW6.4 cells
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                                                                                                                                                             Local
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 QVALENCSAVADTRCGCKPGWFVECQVS-QC 141
                                                                       GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 111
                      EVEI-NCTRTQNTKCRCKPNFFCNSTVCEHC 143
                                                                                                                                            h 5.8%;
Similarity 34.1%;
31; Conservative
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J. Biol. Chem. (1992) 267:10709-10715
Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas
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apoptosis-mediating surface
surface antigen APO-1
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S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Na
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17-Jan-1992 #sequence_revision 17-Jan-1992
10-Sep-1997
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#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label TMM
#th 335 #molecular-weight 37732 #checksum 4899
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Pred. No. 3.26e-14;
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J.; Trauth,
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Best Local Similarity 30.9%;
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106-147
66,181,205,238
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                                                                                                                                          #description
##residues 1-349 ##label KOL
##cross-references EMBL:X67117; NID:g516428; PID:g516449
##experimental_source strain India-1967, isolate Ind3
                                                                                                                                                                                                                                         ##experimental_source strain India-1967, ssp. major, isolate Ind3.NCE S46868
                                                                                                                                                                                                                                                                            ##residues 1-349 ##label BLI ##cross-references GB:X69198; NID:g456758; PID:g457087
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##cross-references GB:M95181; GB:
PID:g332310
                                                           ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PCKNETFTA-STNHAPACVSCRGRCTGHLSE-S-QSCDKTRDRVCDCSAG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLLVLLGARAQGGTR-SP-RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLLLAYVACVYGGGAPYGADRGKCRGNDYEKDGL-CCTSCPPGSYASRLCG-PGSDTVCS 62
                                                                                                                 Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sandakhchiev, I.S. submitted to the EMBL Data Library, April 1992
Nucleotide sequence analysis of the region of variola virus XhoI F O H P Q genome fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D36858 #type complete
gene G4R protein - variola virus
B28R protein (COP)
                                                                                                                                                                                                                                                                                                                                                               D36858
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                                                                                                                                                                                                                                                                                                                                                                                  not shown.
                                                                                                                                                                                                                                                                                                                                                                                                    submitted to GenBank,
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                                                                                                     S46888
                                                                                                                                                                                                                                                                                                                                                                                                                                                              D36858; S46888; S32385; S35987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name variola virus
30-Sep-1993 #sequence_revision
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T2 protein - myxoma virus
#formal_name myxoma virus
31.pec-1992 #sequence_revision 31-Dec-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                           Blinov, V.M.
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Virology (1991) 184:370-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A40566
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#domain NGF receptor repeat homology #label
#binding_site carbohydrate (Asn) (covalent)
                                                                                preliminary
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Pred. No. 7.40e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                      November 1992
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. NG3\
#status
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REFERENCE
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Best Local :
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#journal
#title
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#journal FEBS Lett. (1993) 319:80-83
#title Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.
#accession commons.
#map_position 12p13-12p13
#introns 46/1; 90/1;
                                                      #gene
                                                                                                                                                                                                                        growth factor/tumor necrosis factor #cross-references MUID:92013149
                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title Genomic organization and chromosomal human CD27 gene.
#cross-references_MUID:93094588
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                                                                                                                                        ##cross-references GDB:132582;
                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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##cross-references EMBL:X69198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 TFLAWENHHUSECARCQA-CDEQASQVALENCSAVADTRCGCKPGWF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 IIINGRDAAPYTPPNGKCKDTEY-KRHNL-CCLSCPPGTYASRLC-DSKTNTQCTPCGSG
                                                                                           soluble CD27 found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 5.5%;
Similarity 27.1%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A46517 #type complete
CD27 antigen precursor - human
CD27L receptor; T cell activation antigen CD27
#formal_name Homo sapiens #common_name man
18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change
22-Jun-1999
                                                                                                                                                                                                                                                           Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B. J. Immunol. (1991) 147:3165-3169
The T cell activation antigen CD27 is a member of the nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loenen, W.A.; Gravestein, L.A.; Beumer, Hagemeijer, A.; Borst, J. J. Immunol. (1992) 149:3937-3943
                                                        GDB:CD27
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#length 349
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                                                                                                                              sequence extracted
                                                                                                                                                                                                                                                                                                                                      authors propose an alternative repeat pattern
                                                                                                                                                                                                                                                                                                                                                         sequence extracted from NCBI backbone (NCBIP:120386)
                                                                                                                                                                                                                                                                                                                                                                           1-260 ##label LOE
                                                                                                                                                                                                                                                                                                                                                                                                            not compared with conceptual translation
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NGF receptor repeat homology #label
#molecular-weight 38189 #checksum
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                                                                                           in serum and urine
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Pred. No. 2.36e-12;
27; Mismatches 43
                                     OMIM:186711
                                                                                                                              from NCBI
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                                                                                           is
                                                                                                                            backbone (NCBIN:60285)
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Best Local
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121-188
192-211
212-260
95
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21-260
21-191
27-63
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211-235
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                                 118 CSAVADTRCGCKPG 131
                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X17037; NID:957830; PID:957831
FICATION #superfamily CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 5.4%;
Local Similarity 25.2%;
hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
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                                                                   94
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                                                                                                                                         37 CCRECQPGHGMVSRC-DHTRDTVCHPC-EPGFYN-EAVNYDTCKQCTQCNHRSGSELKQN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 LVC-PQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PHPWWLCVLGTLVGLSATPAPK-SCPERHYWAQGKLCCQMCEPGTFLVKDCDQHRKTAQC
                                                                   CTPTEDTVCQCRPG 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPCIPGVSFSP-DHHTRPHCESCRHCN--SGLL-VRNCTITANAECACRNGW--QCRDKE 116
                                                                                                       CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQALLLVLLGA-RAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OX40 antigen precursor - rat
nerve growth factor receptor tomolog
#formal_name Rattus norvegicus #common_name Norway rat
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes - a molecule related to nerve gr factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily CD27 antigen; NGF receptor repeat homology
duplication; glycoprotein; homodimer; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                            growth factor receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      S12783
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S12783
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#product OX40 antigen #status predicted #label MAT\
#product OX40 antigen #status predicted #label TMM
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Pred. No. 5.09e-12;
36; Mismatches 50;
                                                                                                                                                                           Score 165; DB 2;
Pred. No. 4.82e-10;
17; Mismatches 32
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Similarity 30.0%;
33; Conservation
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Kohno, T.; Bre
M.W.; Hale,
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M.P.; Jerzy, R.; Dower, S.K.; Cosman, D.; 
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##cross-references EMBL:X85214; NID:g732818; PID:g732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HPC-ETGFYN-EAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPG 108
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Claassen, E.; Noelle, R.J.; Fell, H.P.
J. Immunol. (1993) 151:5261-5271
Cloning of mouse Ox40: a T cell activation
mediate T-B cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75K tumor necrosis factor receptor #formal_name Homo sapiens #common_name man 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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Eur. J. Immunol. (1995) 25:926-930

Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.
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th 272 #molecular-weight 30153
                                                                        Brewer, M.T.;
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protein - mouse
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Pred. No. 2.27e-10;
22; Mismatches 49; Indels
                                                                                                                                                                                   NID:g189185; PIDN:AAA59929.1; PID:g189186
                      Squires,
           Baker, S.L
S.L.; SCnwar,
H.; Thompson,
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                                                                              Schwartz,
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                                 R.C.
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                                                                              P.E.;
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#title Purification and partial amino acid sequence analysis of two
distinct tumor necrosis factor receptors from HL60 cells.
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#title
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#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155

#title Complementary DNA cloning of a receptor for tumor necrosis
factor and demonstration of a shed form of the receptor.

#cross-references_MUID:90349572
                                                                                                                                                    receptor encoding gene (TNF-R).
                                                                                                                                                                                                                                                                                                                                                                                            #accession
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                                        ##residues 1-37 ##label RES 1-37 ##label RES
                                                                                                                                                                                                                                                                                                                  ##molecule_type protein
##residues 27-31 ##label ENG
                                                                                                                                                                                                                                                                                                                                                                  ##status
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##residues 23-40;65-69;136-141;300-306 ##label LOE
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##residues 23-461 ##label DEM
##cross-references GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
##cross-reference extracted from NCBI backbone (NCBIN:63368,
##note
                                                                                 ##molecule_type DNA
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Gene (1994) 150:381-386
Cloning, sequencing and partial functional characterization
of the 5' region of the human p75 tumor necrosis factor
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J. Biol. Chem. (1990) 265:1531-1336
Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity
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Gentz, R.; Brockhaus, M.; Lesslauer, W.
Cytokine (1990) 2:231-237
Two human TNF receptors have similar extracellular,
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KEYWORDS
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Best Local Similarity 27.6%;
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     DEQASQVALENCSAVADTRCGCKPGWF 133
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#superfamily tumor necrosis factor receptor type 2;
receptor repeat homology
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#length 461 #molecular-weight 48291 #checksum 5724
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#product tumor necrosis factor receptor type 2 #status
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Pred. No. 1.56e-10;
19; Mismatches 37; Indels
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Search completed: Tue Jul 25 22:21:58 2000 Job time: 27 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

\* \*

Run on: MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Tue Jul 25 22:20:36 2000; MasPar time 36.30 Seconds 817.386 Million cell updates/sec

Description: Perfect Score: (1-428) from US09314889.pep >US-09-314-889-2 Tabular output not generated.

Sequence: 1 MEETQQGEAPRGQLRGESAA.....ERMGLDGCVEDLRSRLQRGP 428

Searched: Scoring table: PAM 150 Gap 11

225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_archea 2:sp\_bacteria 7:sp\_mhc 8:sp\_organelle
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 47.496; Variance 85.662; scale 0.554

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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DT 01-JAN-1998 (TrEMBLrel. 0)
DT 01-JAN-1998 (TrEMBLrel. 1)
DT 01-OV-1999 (TrEMBLrel. 1)
DE DEATH RECEPTOR 3 BETA.
GN DA3.
OS Homo sapiens (Human).
CU Eukaryota; Metazoa; Chordi
OC Eutheria; Primates; Catar;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98113360.
RA MARZOCHA K., RIBEIRO P., (
RA WARZOCHA K., RIBEIRO P., (
RA BALLES G.;
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RL EMBL; AFO26070; AAC39556.
DR HSSP; P19438; ITNR.
DR PFAM; PF00020; TNFR_NG
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DR PFAM; PF00020; TNFR_NG
DR PFAM; PF00031; death; 1.
DR PFAM; PF00031; death; 1.
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EMBL; AF026070; AAC39556.1; -.
HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR_1;
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                                              GLREAEIEAVEVEIGLFRDQQYEMLKHWRQQQPAGLGAVYAALERWGLDGCVEDLRSRLQ
                                                                                           TADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCP
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Best Local
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SEQUENCE FROM N.A.

MEDITARE: 97372273.

SCREATON G.R., XU X.N., OLSEN A.J

MCMICHAEL A.J., BELL J.I.;

*LARD: a new lymphoid-specific do

regulated by alternative pre-mRNJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O00279 PRELIMINARY; PRT; 372 AA.
O00279;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence up
O1-NOV-1999 (TrEMBLrel. 12, Last annotation
LYMPHCTYE ASSOCIATED RECEPTOR OF DEATH 8
                                                                                                                                                                                                                                                                                                                                                   000280 PRELIMINARY; PRT; 380
000280;
01-JUL-1997 (TrembLrel. 04, Created)
01-JUL-1997 (TrembLrel. 04, Last sequenc
01-NOV-1999 (TrembLrel. 12, Last annotat
LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00531; death; 1.
Alternative splicing.
SEQUENCE 372 AA; 40391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1997) to the EMBL; U94509; AAC51314.1; -. EMBL; U94506; AAC51311.1; -. HSSP; P19438; 1TNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM SCREATON G., )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGP
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ch 75.0%;
l Similarity 98.5%;
321; Conservative
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                                                                                                                                                                                                                                                    Chordata; Craniata; Catarrhini; Hominid
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                                                                                                             OLSEN A.L., COWPER A.E.,
       pre-mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2451; DB 4;
Pred. No. 0.00e+00;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
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       death domain c
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                                                                                                                                                                                                                                                caniata; Vertebrata;
Hominidae; Homo.
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Matches
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Best Loc
Matches
                                                                                                                                                                                                                                                                  ON0276 PRELIMINARY; PRT; 253 AA. 000276; O1-JUL-1997 (TrEMBLrel. 04, Created) O1-JUL-1997 (TrEMBLrel. 04, Last sequence up 01-NOV-1999 (TrEMBLrel. 12, Last annotation LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                      "LARD: a new lymphoid-specific death domain conta regulated by alternative pre-mRNA splicing."; Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997). EMBL; U94503; AAC51308.1; -. BENGITHE ROCKET. FURTHER PROCESS.
                                                                                        PROSITE; PS00652; TNFR_NGFR_1; PFAM; PF00020; TNFR_C6; 2. SEQUENCE 253 AA; 26934 MW;
                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE: 97272273.
SCREATON G.R., XU X.N., OL
MCMICHAEL A.J., BELL J.I.;
                                                                                                                                                                                                                                        Eutheria; Primates;
                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. EMBL; U94510; AAC51315.1; -. HSSP; P19438; ITNR. HSSP; P19438; PROSITE; PS00652; TNFR_NGFR_1;
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PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                   PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSWDQL
                                                                                                                                                                                                                                                                                                                                                                           VEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSCPERCAAVCGWRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTST
                                                                                                                                                                                                                                                                                                                                                                                                                        PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAETEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00531; death; 1.
PF00020; TNFR_c6; 2.
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 AA;
                                           45.8%;
larity 95.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                       TNFR_c6; 2.
AA; 26934
                                                                                                                                                                                                                                       Chordata; Craniata; Ve
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41192 MW;
                                                                                                                                                                                           OLSEN
                                           Score 1497;
Pred. No. 0.
3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2403; DB 4;
Pred. No. 0.00e+00;
                                                                                                                                                                                           A.L.,
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                                                                                        CRC32;
                                                                                                                                                                                                                                                  Vertebrata;
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Best Loc
Matches
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01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                           000278 PRELIMINARY;
000278;
01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-NOV-1998 (TrEMBLrel. 08,
"LARD: a new lymphoid-specific death domain cont regulated by alternative pre-mRNA splicing."; Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997) EMBL; U94508: AAC51313.1; -. PFOMS51; death; 1. SEQUENCE 234 AA; 25373 MW; 272FD3C9 CRC32;
                                                                                                                                                                                                                                        LYMPHOCYTE ASSOCIATED RECEPTOR OF Eukaryote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1997) to the EMI
EMBL; AF026071; AAB82288.1; -
HSSP; P19438; ITMR.
PROSITE; PS00652; TMFR_NGFR_1;
PFAM; PF00020; TMFR_C6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 6
014866
                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 97272273.
SCREATON G.R., XU X.N., OL
MCMICHAEL A.J., BELL J.I.;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGSCPERCAAVCGWRQSRW
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NCE 277 AA;
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; Metazoa; Chordata; C:
Primates; Catarrhini;
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AA; 29111 MW;
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                                                                                                                                      A.L.,
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i; Hominidae;
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annotation
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No. 1
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L.19e-271;
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Best Local Similarity
Matches 59; Conser
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Best Local Similarity 100.0%;
Matches 182; Conservative
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLREL. 08, Last annotation update)
                                                                                                                                      O19131 PRELIMINARY;
019131;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                        "LARD: a new lymphoid-specific death domain containing regulated by alternative pre-mRNA splicing."; proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997). EMBL; U94507; AAC51312.1; SEQUENCE 126 AA; 13349 MW; B4B4851A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 97272273.
SCREATON G.R., XU X.N., OL
MCMICHAEL A.J., BELL J.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                             Eutheria;
Bovinae; E
                                                                                                                     UI-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TUMOR NECROSIS FACTOR-RECEPTOR I.
SEQUENCE FROM N.A.
TISSUE-AORTA;
LEE E.-K., TALYOR M.J.,
Submitted (FEB-1997) to
                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYMPHOCYTE ASSOCIATED RECEPTOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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                                                                                                                                                                                                                                           RLLC
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llarity 92.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLSEN A.L., COWPER A.E.,
 KEHRLI M.E.;
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1329; DB 4;
Pred. No. 2.14e-268;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         Score 467; DB 4;
Pred. No. 2.63e-72;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                           Vertebrata; Mammalia;
Pecora; Bovoidea; Bovi
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  databases
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                                                                            Bovidae;
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Matches 3
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Best Local
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HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR_1; 3
PRAM; PF00531; death; 1.
PFAM; PF00020; TNFR_C6; 3.
SEQUENCE 471 AA; 51367 MW; 1
                                                                                                                                                                                                                 TLT 10
097491;
097491;
01-MAY-1999
01-MAY-1999
01-NOV-1999
FAS PROTEIN.
                                                                           SEQUENCE FROM N.A.
TISSUB-LYMPHOCYTE;
TAKAGI M., TAKAHSHI H., KABEYA H., OHASHI K.,
"Cloning of sheep fas antigen.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AB011671; BAA37093.1; -.
                                                                   EMBL;
HSSP;
                                                                                                                                                                  Caprinae;
                                              SEQUENCE
                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                    331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESPCP-QGKYNHPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLRR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIPCQ---ERQDTIC-HCHMGFFLKGAKCISCHDCKNKECEKLCPTRPSTGKDSQDPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLLAGLVV-PL-LLG-ATLTYTYR-HCWPHK--PLV----T-ADEAGMEALTP-P---PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLLPLVIVFGLCLASFASVVLACRYQRWKPKLYSIICGQSTLVKEGEPELLVPAPGFNPT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
                                                                                                                                                                                                                                                                                                                                                                            VRRLGLSEHEIERLELENGRHLREAQYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCL 450
                                                                                                                                                                                                                                                                                                                                                                                                              -LPSRA-L---GPAAAPTL-SP----ESPA-GSPAMMLQPGPQ-LYDVMDAVPARRWKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGAL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CLSCSRCRDEMFQVEISPCVVDRDTVCGCRKNQYREYW-GE-TGFRCLNCSLCPN-GTV 154
                                                                                                                                                                                                                                                                                                                      EDLRSRL
                                                                                                                                                                                                                                                                                                                                           ENIEEAL 457
                                                                                                                                                                                                                                                                                                                                                                  GPPASTHLCTPGPPASTHLCTPVQKWEASAPSAPDQLADADPATLYAVVDGVPPSRWKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           THL--SPLDSAHTLLAPP-DSSEK--ICTVQLVGNSWTPGYPETQEALC-PQVTWSW-DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTICFSSTPSSSPVSIPPYISCDRSNFGAVASPSSETAPPHLKAGPILPGPPASTHLCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAA-VC-GW-RQMFWVQ
                                          P25445; 1DDF.
TE; PS00652; TNFR_NGFR_1;
NCE 327'AA; 36928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sch 8.3%;
il Similarity 30.0%;
128; Conservative
h 6.7%;
Similarity 30.2%;
32; Conservative
                                                                                                                                                           Cetartiodactyla;
Ovis.
                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                              10,
10,
12,
Score 218;
Pred. No. 1.
23; Mismatcl
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79; 1
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Last sequence up
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Pred. No. 2.91e-31;
                                                                                                                                                                                                                                                                          PRT;
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                                              1.
67261BB8
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  Mismatches
                                                                                                                 OHASHI K.,
                                                                                                                                                                                                                                                                           327
                                                                                                                                                                        Pecora; Bovoidea; Bovi
                       DB 6;
                                               CRC32;
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  44;
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                                                                                            databases
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                        Length
                                                                                                                 SUGIMOTO C.,
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  Indels
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Best Loc
Matches
Query Match
Best Local Similarity
                                                                               PROSITE;
Receptor.
NON_TER
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01-MAY-1999
01-NOV-1999
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097530;
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                                                                                                                                        DUTHIE S., NASIR L., ARGYLE D.J., ECKER. Canine tumor necrosis factor receptor, submitted (JUL-1997) to the EMBL/GenBanl EMBL, AF013955, AADO1516.1; -. HSSP; P19438; 1TNR.
                                                                                                                                                                                                                                           TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
Canis familiaris (Dog)
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALIBERT L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANDERSON D.M., MARASKOVSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANK.
Homo sapiens (Human).
Chordata;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLCALLARLQVALQIAPPCTSEKHYEH-LGR-CCNKCEPGKYMSSKCTTT-SDSVCLPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQDTFL-AWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPDEYLDSW-NEEDK-CLLHKVCDTGKALVAVVAGNSTTPRRCACTAG-YHWSQDCECCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLVLLGARAQGGTR-SPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                       PS00652;
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                                                          189
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TIEMBLIE1 12, Created)
(TIEMBLIE1 12, Last sequence update)
(TIEMBLIE1 12, Last annotation updat
(TIVATOR OF NUCLEAR FACTOR-KAPPA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MARASKOVSKY E.,
                                                                                                                   TNFR_NGFR_1;
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                                                          189
21324
  6.4%;
                                                                                                                                                                                                                                                                                                                            Chordata;
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                                                                                                                                                                                                                                                                                                       Fissipedia;
                                                            MW;
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  Score 210;
Pred. No.
                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 213; DB 4; Lei
Pred. No. 1.01e-19;
29; Mismatches 65;
                                                                                                                                                                                                                                                                                                   Craniata; Vi
ia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BILLINGSLEY W.L., D
E M.C., DUBOSE R.F.,
                                                            24A93EBF
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                                                                                                                                                                                                   ECKERSALL P.D.;
eptor, partial c
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  3.74e-19;
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                                                            CRC32;
                                                                                                                                                                                                                                                                                                                      Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
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095185; O1-FEB-1997 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
FAS ANTIGEN SPLICED VARIANT.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                              ISONO T., TANBE Y., NAGANO Y., SETO A.; "Splicing and allelic variation in the rabbit Submitted (DEC-1998) to the EMBL/GenBank/DDBJ EMBL; AB021297; BAA78429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U72344; AAB95089.1; -. HSSP; P19438; 1EXT. PROSITE: BEADER.
                                            SEQUENCE
                                                                                                                                                                                           Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                    Q9XS60
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              Q9XS60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNGTVQISCKETQNTVC-TCHAGFFLRGNECVSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGA-
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larity 31.8%;
Conservative
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                                          30374 MW;
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    6.2%;
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RECEPTOR P60
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                                          43BF129F
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  202;
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No. 2.12e-18;
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RESULT 15
ID 09XS29
AC 09XS29,
DT 01-NOV-1
DT 01-NOV-1
DT 01-VV-1
DF C-TYPE F
OS Oryctola
OC Eutharyotol
OC Eutharia
RN [1]
RN [1]
RN [1]
RN SEQUENCE
RA ISONO T.
RT "Splicir
RI Submitte
DR EMBL; AL
DR EMBL; AL
DR EMBL; AL
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Search completed: Tue Jul 25 22:21:15 2000 Job time : 39 secs.
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Best Local Similarity 34.0%;
Matches 32; Conservative
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Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

ISONO T., TANBE Y., NAGANO Y., SETO A.;

ISONO T., TANBE Y., NAGANO Y., SETO A.;

"Splicing and allelic variation in the rabbit Fas antigen gene.";

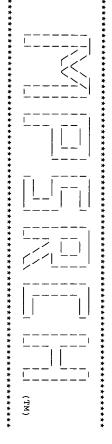
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB021299; BAA78431.1; -.

EMBL; AB021296; BAA78428.1; -.

EMBL; AB021296; BAA78428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
C-TYPE FAS ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 VALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 146
                                                                                                        100 VETD-CTTIQNTKCRCKSNFF--CNALKCEHCDP 130
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                                                                                     113 VALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 146
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                                                                                                                                                                                              41 GNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTD-KSHFSSKCRRCSLCDGEHGLE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                       Score 202; DB 6; Length 320; Pred. No. 1.19e-17; 19; Mismatches 37; Indels
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19; Mismatches 37;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:20:00 2000; MasPar time 15.22 Seconds 871.530 Million cell updates/sec

Tabular output not generated.

Title: >US-09-314-889-2
Description: (1-428) from US09314889.pep
Perfect Score: 3267

Perfect Score: 3267
Sequence: 1 MEETQQGEAPRGQLRGESAA....ERMGLDGCVEDLRSRLQRGP 428

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 48.842; Variance 83.135; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

20 21 22 23	13 15 17 18	110 111 112	 Januaran	Result No.
	177 165 167 168 164		407 399 398 383 278 213	Sc
4.9	5.11 5.11 4.9	51 51 51 51 51 51 51 51 51 51 51 51 51 5	12.5 12.2 12.2 11.7 6.5	Query Match
474 474 415 656	260 271 272 461 325 277	324 327 335 326 349	455 461 332 332	1 ~
				DB
TNR2_MOUSE CD27_MOUSE TNRC_MOUSE RIP_MOUSE	CD27_HUMAN OX40_RAT OX40_MOUSE TNR2_HUMAN VT2_SFVKA CD40_HUMAN	FASA_RAT FASA_MOUSE FASA_HUMAN VT2_MYXVL VC22_VARV	TNR1_HUMAN TNR1_MOUSE TNR1_PIG TNR1_RAT FASA_PIG FASA_BOVIN	ID WSL1_HUMAN
TUMOR NECERCORSIS FACTOR CD27L RECEPTOR PRECURS LYMPHOTOXIN-BETA RECEP SERINE/THREONINE PROTE	CD27L RECEPTOR PRECURS OX40L RECEPTOR PRECURS OX40L RECEPTOR PRECURS TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR CD40L RECEPTOR PRECURS LYMPHOTOXY N.BETOR RECURS	RECEPTOR RECEPTOR RECEPTOR R NECROSIS	TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR FASL RECEPTOR PRECURSO FASL RECEPTOR PRECURSO	Description WSL-1 PROTEIN PRECURSO
1.31e-09	5.28e-14 8.94e-12 3.84e-12 2.51e-12 1.36e-11 1.10e-10	1.37e-20 3.32e-19 1.77e-16 6.00e-15 2.22e-14	9.43e-63 6.00e-61 1.01e-60 2.35e-57 2.14e-34 5.49e-21	Pred. No.

4.5	43	42	41	40	39	38	37	36	ა 5	34	ω ω	32	31	30	29	28	27	26	25	24
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1789 3707	1245	883	647	612	400	103	103	1609	1607	655	289	269	1247	277	799	3635	425	671	427	416
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LMB1_DROME PGBM_MOUSE	NIDO_MOUSE	PGCB_MOUSE	GAG_SFV1	OCTC_RAT	LMB_HIRME	VA53_VACCV	VA53_VACCC	LMG1_HUMAN	LMG1_MOUSE	ITB5_PAPCY	CD40_MOUSE	CD40_BOVIN	NIDO_HUMAN	OX40_HUMAN	ITB5_HUMAN	LMA5_MOUSE	NGFR_RAT	RIP_HUMAN	NGFR_HUMAN	NGFR_CHICK
LAMININ BETA-1 CHAIN P BASEMENT MEMBRANE-SPEC	NIDOGEN PRECURSOR (ENT	BREVICAN CORE PROTEIN	GAG POLYPROTEIN (CORE	PEROXISOMAL CARNITINE	LAMININ B-CHAIN (FRAGM	PROTEIN A53.	PROTEIN A53.	LAMININ GAMMA-1 CHAIN	LAMININ GAMMA-1 CHAIN	INTEGRIN BETA-5 (FRAGM	CD40L RECEPTOR PRECURS	CD40L RECEPTOR PRECURS	NIDOGEN PRECURSOR (ENT	OX40L RECEPTOR PRECURS	INTEGRIN BETA-5 PRECUR	LAMININ ALPHA-5 CHAIN	LOW-AFFINITY NERVE GRO	SERINE/THREONINE PROTE	LOW-AFFINITY NERVE GRO	LOW-AFFINITY NERVE GRO
2.22e-02 2.22e-02		4.37e-02	3.12e-02	3.12e-02	2.22e-02	3.12e-02	3.12e-02	7.95e-03	1.12e-02	1.12e-02	1.58e-02	1.58e-02	3.96e-03	3.96e-03	1.96e-03	1.08e-04	7.88e-06	2.50e-06	3.59e-07	2.24e-08

# ALIGNMENTS

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Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
(NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "TRAMP, a novel apoptosis-mediating receptor with sequence to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)."; Immunity 6:79-88(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bodmer J.-L., Burns K., Schneider P., Hofmann Thome M., Bornand T., Hahne M., Schroeter M., Browning J.L., Macdonald H.R., Tschopp J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97272273.
Screaton G.R., Xu X.-N.,
MCMichael A.J., Bell J.I
                                                                                                           PROSITE;
                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                   EMBL;
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MEDLINE; 97205335.
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                                                                                                                                                                                                                                                                           EMBL;
                                                                                             Receptor;
                                                                                                                                     PROSITE; PS00652;
                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: THREE ISOFORMS; WSL-1/LARD-1A (SHOWN HERE),
WSL-SL/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
PTM: GLYCOSYLATED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAPLAT A ROLE IN REGULATING LYMHOCCYTE HOMEOSTASIS.

SUBUNIT: HOMODIMER, INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFRI-ASSOCIATED MOLECULE TRADD AND THE TNRFI RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: GLYCOSYLATED (PROBABLE).
SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                 Y09392; CAA70561.1;
Y09392; CAA70559.1;
Y09392; CAA70560.1;
Y09392; CAA70560.1;
U72763; AAC50819.1;
U83599; AAB41434.1;
U83599; AAB41435.1;
U74601; AAB4918.1;
U74611; AAB49714.1;
U74611; AAB49714.1;
U74611; AAC51306.1;
U94504; AAC51309.1;
U94504; AAC51309.1;
U94504; AAC51192.1;
U75380; AAC51192.1;
U75381; AAC51193.1;
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U75381;
U83597;
P19438;
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PS50017;
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TNFR_NGFR_2; 1.
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4 X TNFR-CYS.
                         POTENTIAL.
WSL-1 PROTEIN.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                              Transmembrane;
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P19438;
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O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
O1-FEB-1991 (Rel. 17, Last sequence update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
TNPRSF1A OR TMER1 OR TNFAR.
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L->A: SUPPRESSES HOMODIMERIZATION, T
INTERACTION, AND APOPTOSIS INDUCTION
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MEALTPPPATHLS -> SRWCAGNARGRTGMDRGEAGEEGG
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STLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGA ->
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Schall T.J., Lewis M., K
Getanaga T., Granger G.A
"Molecular cloning and e
necrosis factor.",
Cell 61:361-370(1990).
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                                                                                                                                                                                                                                                MEDLINE; 9
                                                     Broger C., Loetscher H., Lesslauer W.; "Crystal structure of the soluble human beta complex: implications for TNF recep
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Tabuchi H., Lesslauer W.;
"Molecular cloning and expression
factor receptor.";
Cell 61:351-359(1990).
                                                                                                                                      Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell su
tumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                          Gray P.W., Barrett K., Chantry D., Turner M., Feldman M. "Cloning of human tumor necrosis factor (TNE) receptor c expression of recombinant soluble TNF-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
                                                                                                                                                                                                                                                                                                                                                                     Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
DNA Cell Biol. 9:705-715(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          soluble form, encodes both receptor.":
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"Soluble forms of tumor necrosis factor receptors
for the type I TNF-R, cloned using amino acid sequ
             MEDLINE;
                        X-RAY
                                                                                     Banner D.W.,
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MEDLINE; 91017509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                      Structure
                      CRYSTALLOGRAPHY (1.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9:3269-3278(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
90235284.
 97094982.
                                                                                                                                                                                  90110215.
                                                                                                                                                                                                                                                          FROM N.A.
92250049.
                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
91090841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A., AND 91006021.
                                                                                                                                                                                                                  13:219-224(1992).
                                                                                                 93258809
                                                                                                                                                                                                                          Strehl S., Dworzak M., Himmler A., e of the human TNF receptor 1 (p60) ion to chromosome 12p13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90235285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                    D'Arcy A.,
  Devine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates;
  T.O.,
                                                                                                         (2.85 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brakebusch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [F]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koller K.J., Lee A., Rice G.(A., Lentz R., Raab H., Kohr Verpression of a receptor for
                                                                                     Janes W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
 Khono H.,
                       ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sing amino acid sequence cell surface and a solu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         С.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF.
                                                                                     Gentz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41-53; 110-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Engelmann H.,
Sprang S.R.
                       OF.
                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gentz
                                                                                   R.,
                                                                55 kd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
                       41-202
                                                                                                         30-211
                                                      activation
                                                                                     Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.,
                                                                                                                                                                                                                                     gene
                                                                TNF
                                                                                                                                                                                                                                               Ambros P.F.;
                                                                                                                                                                                                                                                                                                                          Feldman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brockhaus
                                                                receptor-human
                                                                                                                                                                                                                                    (TNFR1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TNF-RS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .C., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zwang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis
                                                                                                                                                                                                                                                                                                               CDNA
                                                                                    H.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong G.H.W.,
, Goeddel D.V.;
                                                                                                                                                  cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA
                                                                TNF
 CHAIN
                                                                                                                                                                                                      PFAM;
                                                                                    DOMAIN
                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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Structure 4:1251-1262(1996)
-i- FUNCTION: RECEPTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structures of the extracellular factor receptor.";
NF-KAPPA B SIGNALING.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
SIMILARITY: CONTAINS A LA-NGFF/TNFR-TYPE CYSTEINE-RICH REGION.
DATABASE: NAME-PROW; NOTE-CD guide CD120a entry;
NWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR TWF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH INUCLING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYTOCIDAL TWF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPLINGOMIYELINASE.
                                                                                                                                                                                                                                                                                                                                                                                            WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THI HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPEC
                                                                                                                                                                                                                                                                                                                                                             ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIFICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR1 LEADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAINS
                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                   TC
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modified and this statement is not removed the European SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM an email to license@isb-sib.ch). requires a non. Bioinformatics Institute. The profit institutions as long license agreement (See http://www.isb-sib.ch/announce/ There are no restrictions ng as its content is in Usage ьy and EMBL outstation a for collaboration n no way on no

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DOMAIN
DISULFID
               DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
DOMAIN
                                                                      DOMAIN
TRANSMEM
                                                                                                              3D-structure.
                                                                                                                     Receptor;
                                                                                                                              PROSITE;
                                                                                                                                                                                          A35010;
S12057;
S1208;
A38208;
1TNR; 31
                                                                                                                                                                                                                                  X55313; CAA39021.1;

M33294; AAA03210.1;

M58286; AAA36753.1;

M63121; AAA36754.1;

M75866; AAA61201.1;

M75864; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61251.1;
                                                                                                                                                                                                                           A34899;
                                                                                                                                                           PF00020; TNFR_c6;
                                                                                                                                                     PF00531; death;
                                                                                                                             PS50050;
PS50017;
                                                                                                                                              PS00652;
                                                                                                                   Transmembrane;
                                                                                                                                                                           31-JUL-94
07-DEC-95
11-JAN-97
A38208
                                                                                                                                                                                                                           GQHUT1.
                                                                                                                                                                                                            S12057
                                                                                                                                                                                                                    A35010.
                                                                                                                              DEATH_DOMAIN;
                                                                                                                                   TNFR_NGFR_1;
TNFR_NGFR_2;
21
455
291
211
234
455
196
196
196
348
441
                                                                                                                                                            4.
                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                 JOINED.
                                      TNFR-CYS
                                                      CYTOPLASMIC (
               N-SMASE
                       TNFR-CYS
                               TNFR-CYS
                                                                       POTENTIAL
                                                                             TUMOR NECROSIS
                                                                                                                                     ωω
                                                                                     NECROSIS
NECROSIS
        DOMAIN
               ACTIVATION DOMAIN (NSD)
                         4
                                                                                                                     Repeat;
                                                               (POTENTIAL)
                                                                             S FACTOR RECEPTOR 1
S FACTOR BINDING PROPOTENTIAL).
                                                                                                                    Signal;
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Apoptosis

PROTEIN

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RESULT RESULT AC EXPENSE OF THE ACC E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
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Best Local S
Matches 12
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DISULFID
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DISULFID
  Wong G.H.
"Cloning
necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID
                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                              P25118;
01-MAY-1992 (Rel. 22,
01-MAY-1992 (Rel. 22,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                              SEQUENCE FROM N.A. MEDLINE; 91187885.
                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                TNFRSF1A OR TNFR1 OR TNFR-1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                               TNR1_MOUSE
                                                                                                                                              Mammalia; Eutheria;
                                        Lewis M., Tartaglia L.A., Lee A., Wong G.H., Chen E.Y., Goeddel D.V.
                                                                                                                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIGLSDHEIDRLEIQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A-LTPPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                LRSRL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GELEGITIKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIENVKGTEDSGTTVLLP-LVIFFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEEAL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
127; Conser
                     and expression of cDNAs for two
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455
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                                                                                                                                                                                                                                                                                                                               STANDARD;
  receptors
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50494
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81
99
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                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.5%;
29.9%;
                                                                                                                                                                                                                                                                                           Created)
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    demonstrate
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POTENTIAL.
POTENTIAL.
MISSING (IN REF. 4).
GPAA -> APP (IN REF.
GPAA -> APP (SPAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 407; DB 1;
Pred. No. 9.43e-63;
81; Mismatches 177
                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                             Bennett G.L.,
                                                                                                                                                                                                                                                                                                                                    454
  one receptor
                       distinct murine tumor
                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177;
                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                               Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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    ş
                                                                                                                                                                  Euteleostomi;
                                                               G.C.,
                                                                                                                                              Murinae;
    species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SCPERC-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

M60468; M59377; X59238; X57796; L26349; M76656; M88067; M76655;

AAA40465.1; AAA40465.1; AAA40465.1;

JOINED.

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MOI. IMMUDOI: 30:165-175(1993).

MOI. IMMUDOI: RECEPTOR FOR THE ALDHA. THE ADAPTOR MOLECULE FADD FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

1. SUBURIT: TWE BINDING TO THE EXTRACELLULAR DOMAIN OF TWEFI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVEID A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO TWEFI COMPLEX BY THEIR ASSOCIATION WITH TRADD, THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NET-KAPPA B SIGNALING (BY SIMILARITY).

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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Goodwin R.G., Anderson D., Jerzy R., Davi
Copeland N.G., Jenkins N.A., Smith C.A.;

"Molecular cloning and expression of the
"Molecular cloning and expression of the
"receptors for tumor necrosis factor.";
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SEQUENCE
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Rothe J.,
                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothe J.G., Brockhaus M., Gentz R.
"Molecular cloning and expression
Immunogenetics 34:338-340(1991).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrett K., Taylor-Fishwick D.A., Cope Gray P.W., Feldmann M., Foxwell B.M.J. "Cloning, expression and cross-linking tumor necrosis factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specific.";
Proc. Natl.
                                                                                                                             entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                          modified
                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            necrosis factor receptor beta gene."; Mol. Immunol. 30:165-175(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of the TNF endothelioma cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=SPLEEN
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                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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91285014.
                                                                                                                                                                       non-profit institutions as long and this statement is not removed
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; AAA39751.1;
; AAA40464.1;
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; CAA40936.1;
; AAA59361.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lesslauer W., Steinmetz M.;
function of the murine tumor
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SIGNAL
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REPEAT
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DOMAIN
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MGD; N
PFAM;
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  379
                   392
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S19021;
                                                                                     SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                             WROMEWYQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                                                                                                              RDSLCP-QGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1314884; TNFRSF1A.
IGR-FRDQQYEMLKRWRQQQP--AG-LGAVYAALERMGLDGCVEDLRSRLQRGP
                 NGRCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENTLEAL-RNP
                                      PAAAPTLSPESPAGS-PAMMLQPG-PQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVE
                                                      SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                                           SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                                                 LPLVILLGLCLLSFIFISLMCRYPRWRPEVYSIICRDPVP-VKEEKAGK-PLTPAPSPAF
                                                                                                                                                      CGALHRHTRLLC-SR--
                                                                                                                                                                       CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL
                                                                                                                                                                                         ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQPCLD
                                                                                                                                                                                                          QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP
                                                                                                                                                                                                                              RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P19438;
                                                                                                                                                                                                                                                                      119;
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 3. PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S16677.
S19021.
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59
62
84
102
105
127
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                         DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                             12.2%;
28.7%;
                                                                                                                                                    -RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG
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                                                                                                                                                                                                                                                                   Score 399;
Pred. No. 6.
79; Mismatc
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N-SMASE ACTIVATION E
DEATH DOMAIN.
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                    \pi
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                             POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                          -> G (IN REF. 6).
0710C2E8C3C2B6D9
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Signal; Apoptosis.
                                                                                                                                                                                                                                                                   DB 1; Le
5.00e-61;
ches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                      Length 454;
                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN (NSD)
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                    Gaps
                                                        391
                                                                          320
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RESULT
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01-OCT-1996 (Rel. 3
15-JUL-1999 (Rel. 3
TUMOR NECROSIS FACT
  DOMAIN
DISULFID
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P50555;
                                                                                                                      REPEAT
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DOMAIN
                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECRUITS CASPASE 8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

1. SUBSUTIT: THE BINDING TO THE EXTRACELULIAR DOMAIN OF THERI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACT'S SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NE-KAPPA B SIGNALING (BY SIMILARITY).

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                  CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.";
Gene 163:263-266(1995)
-!- FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                         EMBL; U19994; AAC48499.1; HSSP; P19438; lTNR.
                                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96011645
Suter B., Pauli U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFRSFIA OR TNFR1.
Sus scrofa (Pig)
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of the cDNA receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     PF00531; death; 1.
TE; PS00552; TNFR_NGFR_1; 3.
TE: PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                             PF00020; TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  PS50017;
                                                                                                                                                                                                                                                    Transmembrane;
   43
126
167
167
340
340
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102
102
1127
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  encoding
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Last sequence update)
Last annotation update)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                         Glycoprotein;
POTENTIAL.
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
N-SMASE ACTIVATION DEATH DOMAIN.
BY SIMILARITY.
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4 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                  EXTRACELLULAR
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                   TNR1_RAT P22934;
                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";
DNA Cell Biol. 9:705-715 (1990).
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTARE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
-!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS
                                                                                                                                                            Himmler A., Maurer-Fo
Lantz M., Olsson I.,
                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                              TNFRSF1A OR TNFR1 OR TNFR-1.
Rattus norvegicus (Rat)
                                                                                                                                         Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.; "Molecular cloning and expression of human and rat tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                            418
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No. 1.01e-60
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                         GDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQN 94
LLPLVIFLGLCLLFFICISLLCRYPQWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASI 272
                    PCLDCGALHRHTRLLCSRRDTDCGT-CLP-GFYEHGDGCVS-C-PTSTLGSCPERCAAVC
                                       VTIPCKE-KONTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAV
                                                             HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQ
                                                                               H-VROCLSCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGT 153
                                                                                                     GTRSPRCD-CA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN
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TNFR_NGFR_2; 3.
DEATH_DOMAIN; 1.
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50969
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29.8%;
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                                                                                                                                                                                     MW.
                                                                                                                                            Score 383;
Pred. No. 2
73; Mismat
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.35e-57;
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                                                                                                                                              185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FACTOR RECEPTOR 1
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                                                                                                                                                                  Length 461;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LICAND KNOWN AS F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FASA_PIG
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REPEAT
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                  PFAM; PF00020;
                                                                                                                                                                                                                                                                                                      EMBL; AJ001202; CAA04596.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                   DOMAIN
                                                                                                                                                     CHAIN
                                                                                                                                                                        SIGNAL
                                                                                                                                                                                         Apoptosis;
                                                                                                                                                                                                                                                                 PFAM; PF00020; TNFR_c6;
PFAM; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of apoptosis-associated genes in hibernating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDICING RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDICING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FAD AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEIEAVEVEIGR-FRDQQYEMLKRWRQQQP----AGLGAVYAALERMGLDGCVEDLRSRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLYGSLNPVPTPAPVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEEMRLLGLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THLSPLDS-AHTL-LAP-PDSSEKICTVQL--V-GNS-WTPGYPETQEALCPQVTWSWDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWRQWFWVQV-LLAGLVVPLL--LGATLTYTYRH-CWPHKPLVTADEAGM--EALTPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEIERLELONGRCLREAHYSMLEAWRRRTPRHEATLDVVGRVLCDMNLRGCLENIRETLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPSRALGPAAAPT-LSP-ESPAGSPAMMLQPG-PQ-LYDVMDAVPARRWKEFVRTLGLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTIGEN) (CD95).
                                                                                                                                                                                                                                                PS00652;
                                                                                                                                                                                                                            PS50050;
                                                                                                                                                                                                             PS50017;
                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long
                                                                                                                                                                                         Receptor;
     17
176
193
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82
126
227
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                                                                                                                                                                                                       TNFR_NGFR_1; 2.
TNFR_NGFR_2; 2.
DEATH_DOMAIN; 1.
     175
192
332
332
164
81
125
164
311
                                                                                                                                                 16 POTENT
332 FASL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                    ω.
                                                      CYTOPLASMIC (
3 X TNFR-CYS.
TNFR-CYS 1.
                     TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                POTENTIAL
                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                     FASL RECEPTOR
                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNOWN AS FASL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heusch G.,
                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Darmer D.; and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAS)
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RESULTANT OF THE PROPERTY OF T
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SEQUENCE
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                                                                                                       CHAIN
                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                          EMBL; U34794; AAC48546.1; HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         modified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of the bovine Fas.";
DNA Cell Biol. 15:227-234(1996).
-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED ADAPTOR MOLECULE FADD RECRUITS CASPASE-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
01-NOV-1997
                                                                                DOMAIN
                                                                                                                       Apoptosis;
SIGNAL
                                                                                                                                                           PROSITE; PS50050; TNFR_NGFR_2; 2
PROSITE; PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P51867;
                                                                                                                                                                                               PROSITE; PS00652;
                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96226401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 QACD-EQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION. ACTIVE CASPASE-8 HITTIATES THE SUBSEQUENT CASCADE CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE APPOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY). SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FALAND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECARC
                                                                                                                                                                                                                    PF00020; TNFR_c6; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae;
                                                                                                                                                                                                                                                                                                                                                                           non-profit
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116
332
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                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation updat
      17
17
171
189
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                                                                                                                                                                                                                                                                                                                                                       -profit institutions as long as its content this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
OF: Glycoprotein; Transmembrane; Ru
16 POTENTIAL.
323 FAGL RECEPTOR.
170 EXTRACELLULAR (POTENTIAL.
180 POTENTIAL.
181 POTENTIAL.
323 X TURFR-CYS.
163 3 X THER-CYS.
                                                                                                                                                                                             TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos.
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116
37592
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Pred. No. 2.14e-34;
21; Mismatches 38
  POTENTIAL.
CYTOPLASMIC (POTENTIAL)
3 X TNFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions
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                                                                                                                                         Repeat;
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Best Local
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING (APO-1 ANTIGEN) (CD95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
DOMAIN
              DOMAIN
TRANSMEM
DOMAIN
                                                                 Apoptosis;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                               PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 198:666-674(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FASA_RAT
DOMAIN
                                                       CHAIN
                                                                                                                                       PFAM;
                                                                                                                                                               EMBL; D26112; BAA05108.1; -.
                                                                                                                                                                                          or send
                                                                                                                                                                                                                     modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura K., Yamamoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variant mRNA species
                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                   ADAPTOR MOLECULE PADD RECRUITS CASPAGE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPAGE-8 PROTECULTIC ACTIVATION. ACTIVE CASPAGE-8 INITIATES THE SUBSEQUENT CASCADE CASPAGES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERRAL TOLERANCE, IN THE ARTIGEN STIMULATED
                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                   SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rat liver."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNCTRTRNTKCRCKSNFF - - CNSSPCEHCNP - - CTTC - EHGIIEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCCOPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTD-KSHHSDKCIRCSICDEEHGLEVE 113
                                                                                                                                       PF00531;
                                                                                                                                                 PF00020; TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 31; Conse
                                                                                                                                                                                           an email to license@isb-sib.ch).
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                                                                                                                                                                                                         requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                       death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a truncated form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakatsuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
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24;
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Pred. No. 5.49e-2
 EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
3 X TNFR-CYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR-CYS
                                                      BY SIMILARITY. FASL RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4D88A90E9E1F4892 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω N
                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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                                          (POTENTIAL)
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                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 323;
                                                                                 Repeat; Signal
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Best Local
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                              SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              UI-NOV-1997 (Rel. 35, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                  Nature 356:314-317(1992)
                                                                                                                                                                                                                                                                                                                            mouse Fas
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                            APT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                       antigen that mediates apoptosis.";
                                                                                                                                                                         Watanabe-Fukunaga
                                                                                                                                                                                                  VARIANT LPR
                                                                                                                                                                                                                        Proc. Natl.
                                                                                                                                                                                                                                    mice.
                                                                                                                                                                                                                                              transposable
                                                                                                                                                                                                                                                                                                                                                   Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                          Watanabe-Fukunaga R.,
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APO-1 ANTIGEN) (CD95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P25446;
                                                                                                                                                                Nagata S.
                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                   Adachi M., Watanabe-Fukunaga
                                                                                                                                                                                                                                                                                                                           "The cDNA structure, expression, mouse Fas antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
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                                                                                                                                                  Lymphoproliferation disorder in mice explained by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                          Aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 NCSEGLYQ-VGPFCCQPCQPGERKVKD-CTTSGGAPTCHPCTEGEEYTDR-KHYSDKCRR 99
                                                                                                                                                                                                                                                                                                                Immunol.
                                                      FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECULTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCAL CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTESSES) MEDIATURG CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTESSES) MEDIATURG
          APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICLDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            OR FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQACDE-QASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC-LDCGALHR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAFCDEGHGLEVE-TNCTRTQNTKCRCKENFY--CNASLC-DHC-YHCTSCGLE-DILEP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCAGDFHKKIGLFCCRGCPAG-HYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                               OF 1-96 FROM N.A. 93189576.
                                                                                                                                                                                      92195401
                                                                                                                                                                                                                                                                                                                                                                          92148151.
                                                                                                                                                                                                                                              transcription ble element in
                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                       Acad.
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124
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                                                                                                                                                                                                                                                                                                                                                  aga R., Brannan
Jenkins N.A., J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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123
163
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114
                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36835
                                                                                                                                                                            Brannan
                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                             unaga R., Nagata S.;
caused by the insertion of an
an intron of the Fas antigen of
   DETECTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 211; DB 1;
pred. No. 1.37e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS
TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                   Nagata
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POTENTIAL.
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                                                                                                                                                                          C.I.,
                                                                                                                                                                                                                                                                                                                                                              C.I.,
                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                        90:1756-1760(1993)
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a S.;
                                                                                                                                                                          Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                        chromosomal assignment
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   TISSUES
                                                                                                                                                                                                                                                                                                                                                               Yonehara S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
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                                                                                                                                                     defects in
                                                                                                                                                                            Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus
   INCLUDING THYMUS
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                                                                      CASCADE
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Best Local
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P25445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
                                                                                                                    APT1
                                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MOV-1997 (Rel. 35, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis;
Disease mu
                      SEQUENCE
                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
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EMBL; S56490; AAB25700.1;
EMBL; S56485; AAB25700.1;
EMBL; S56486; AAB25700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                          Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                    APO-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADI
AND MAYBE TO OTHER CYTOSOLIC ADPTOR PROTEINS.
DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                              sapiens (Human)
                                                                                                                  OR FAS
                                                                                                                                                                                                                                                                                                                               QACDEQASQVALENCSAVADTRCGCKPGWFVECQVS-QCVSSSP
                                                                                                                                                                                                                                                                                                                                                               TLCDEEHGLEVETNCTLTQNTKCKCKPDFYCDSPGCEHCVRCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCSEGLYQG-GPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMD-KNHYADKCRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:95484;
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                                                                                                                                                                                                                                                                                                                                                                                                         DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDT-FLAWENHHNSECARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00020; TNFR_c6;
                                                                                                                                ANTIGEN)
  91309137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00652; TNFR_NGFR_1; 2.
PS50050; TNFR_NGFR_2; 2.
PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit
                                                          Eutheria;
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                                                                          Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
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37418
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Primates;
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27.98;
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                                                                                                                                    ANTIGEN)
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Pred. No. 3.
19; Mismatc
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3 X TNFR-CYS
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TNFR-CYS 1.
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EXTRACELLULAR (POTENTIAL).
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                                                        Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F6BFFC5ACE356EEE CRC64;
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3.32e-19;
3.5 52;
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                                                                          Vertebrata;
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                                                          Hominidae;
                                                                                                                                                    SURFACE
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                                                                          Euteleostomi;
                                                                                                                                                      ANTIGEN
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DOMAIN
CARBOHYD
 SEQUENCE
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REPEAT
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DOMAIN
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                                                                                                                                                                     PROSITE; PS50050;
PROSITE; PS50017;
                                                                                                                                                                                                                                                                PIR;
                                                                                                                                                                                                                                                                           EMBL; M67454; AAA63174.1; EMBL; X63717; CAA45250.1;
                                                                                                                                                                                                                                                                                                            or send
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             CARBOHYD
                                                                                                                DOMAIN
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                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor superfamily.
J. Biol. Chem. 267:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen, a member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh N., Yonehara S., Ishii
Sameshima M., Hase A., Seto
                                              REPEAT
                                                                                                     TRANSMEM
                                                                                                                                                           Apoptosis;
                                                                                                                                                                                                                                                                                                                                                         the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang B., Eberstadt M., Olejniczak E.T., "NMR structure and mutagenesis of the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krammer P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li-Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 226-240;
                                                                                                                                                3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
                                                                                                                                                                                                                                                                                                                                                                                                    WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm"
                                                                                                                                                                                                                                         S24543; S24543.
1DDF; 12-NOV-97.
                                                                                                                                                                                                                                134637;
                                                                                                                                                                                                                                                                A40036; A40036.
                                                                                                                                                                                                         PF00531; death;
                                                                                                                                                                                                                   PF00020; TNFR_c6;
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                                                                                                                                                                                                                                                                                                                                               non-profit
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profit institutions as long
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                                                                                                                                                                        DEATH_DOMAIN;
                                                                                                                                                                                  TNFR_NGFR_2;
                                                                                                                                                                                            TNFR_NGFR_1;
                      16
335
173
190
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37732
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S., Dhein
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                                                      TNFR-CYS
                                                                                                             FASL RECEPTOR. EXTRACELLULAR
                      POTENTIAL.
                                 DEATH DOMAIN
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3 X TNFR-CYS.
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 0139942535111410 CRC64;
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Nagata S.;
cDNA for human cell sur
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s (APO-1/CD95) death
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B.C.,
                                                                                                              (POTENTIAL).
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Ponstingl H.,
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domain.";
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Query Match

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                                                       Query Match
Best Local
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01-APR-1993
15-JUL-1999
                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VT2_MYXVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Upton C., Macen J.L., Schreiber M., McFadden G.;
"Myxoma virus expresses a secreted protein with homology necrosis factor receptor gene family that contributes to
                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. Tuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 184:370-382(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                       SEQUENCE
                                                                                                                                                         REPEAT
                                                                                                                                                                   REPEAT
                                                                                                                                                                            REPEAT
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                              virulence.
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                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                         REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                         A40566; GQVZML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQFCHKPCPPGE-RKARDCTVNGDEPDCVPCQEGKEYTD-KAHFSSKCRRCRLCDEGHGL 113
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               TLLLAYVACVYGGGAPYGADRGKCRGNDYEKDGL-CCTSCPPGSYASRLCG-PGSDTVCS 62
  ALLLVILGARAQGGTR-SP-RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCL
                                                                                                                                                                                                                                                              P19438; 1TNR.
                                                                                                                                                                                                                                                                                   M95181; AAA46632.1; A23729; CAA01688.1;
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                                             5.6%;
Similarity 30.9%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                       Glycoprotein;
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181
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(Rel. 25, Last sequence update)
(Rel. 38, Last annotation updat
SIS FACTOR SOLUBLE RECEPTOR PREC
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Conservative
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NGFR_2; 2.
Repeat; Signal.
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                                                                                         MW;
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18; 1
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Pred. No. 6.00e-15;
23; Mismatches 45
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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TUMOR NECROSIS FACTOR SOLUBLE
4 X INFR-CYS.
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RECEPTOR PRECURSOR
                                                                                                     POTENTIAL
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                                                                                         ABBF027E947292FF CRC64;
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                                                                                                                                                                                                                                                                                                                                           Usage
                                               45;
                                                                  Length 326;
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RESULT 12

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RT PEBS Lett.
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01-AUG-1992 (Rel. 23, Last seque
15-JUL-1999 (Rel. 38, Last annot
CD27L RECEPTOR PRECURSOR (T-CELL
TNERSET OR CD27.
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Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-!- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus
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                                                                                                                                                                                                                         CD27_HUMAN
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PEAM; PE00020; TNFR_NGFR_1;
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EMBL; X67117; CAA47540.1; -.
PIR; D36858; D36858.
PIR; S35987; S35987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93202281.
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  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                   Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                          TFLAWENHHNSECARCOA-CDEQASQVALENCSAVADTRCGCKPGWF
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29; Conser
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PS50050; TNFR_NGFR_2; 2.
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     Chordata;
Primates;
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Pred. No. 2.22e-14;
27; Mismatches 43
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TNFR-CYS 1.
TNFR-CYS 2.
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viruses necessary
     Craniata; V
Catarrhini;
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                              Vertebrata;
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          Hominidae;
                                                                                                      ANTIGEN
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                              Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=MONOCYTES; MEDLINE; 92013149.
                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00652; TNFR_NGFR_1; 1.
PROSITE: PS50050; TNFR_NGFR_2; 1.
T-cell; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M63928; AAA58411.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.; "The T cell activation antigen CD27 is a member of the nerve factor/tumor necrosis factor receptor gene family."; J. Immunol. 147:3165-3169(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P19438; 1NCF
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  141
                         117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATABASE: NAME-PROW; NOTE-CD guide CD27 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
   CVSSSPF 147
                                                                                                                                                                                                                                                                                                                                                                                                                            A46517
                                             LVC-PQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQ
                        CTECDPL 123
                                                                                                       PHPWWLCVLGTLVGLSATPAPK-SCPERHYWAQGKLCCQMCEPGTFLVKDCDQHRKAAQC
                                                                    DPCIPGVSFSP-DHHTRPHCESCRHCN--SGLL-VRNCTITANAECACRNGW--QCRDKE
                                                                                           PQALLLVLLGA-RAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTC
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93094588.
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TNFR-CYS 3.
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3 X TNFR-CYS.
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EXTRACELLULAR (POTENTIAL).
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A -> T (IN REF. 2).
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                                                                                                                                         Mismatches
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                                                                                                                                                               Length 260
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01-APR-1990 (Rel.
01-OCT-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                       PIR; S08036;
PIR; S12783;
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                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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 118
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                      94 CTPTEDTVCQCRPG
                                                                   CCRECOPGHGMVSRC-DHTRDTVCHPC-EPGFYN-EAVNYDTCKQCTQCNHRSGSELKQN
 CSAVADTRCGCKPG
                                             CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN
                                                                                                                                                                                                                                                                                                                                  PF00020; TNFR_c6;
                                                                                                                                                                                                                                                                                                                                               P25942;
                                                                                                                                                                                                                                                                                                                                                                                 X17037; CAA34897.1;
                                                                                         Similarity 29.7%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9:1063-1068(1990)
                                                                                                                                                                                                                                                                                        PS00652; TNFR_NGFR_1; 3.
PS50050; TNFR_NGFR_2; 2.
; T-cell; Antigen; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90214614.
                                                                                                                                        271 AA;
                                                                                                                                                                                                                                                                                                                                                        S08036.
S12783.
                                                                                                                                                                                                                                                                                                                                              1CDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14,
14,
34,
                                                                                                                                                              19
271
210
235
235
271
164
60
102
123
164
                       107
 131
                                                                                                    5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
(SOR (OX40 ANTIGEN) (MRC 0X40).
                                                                                                                                         ¥.
                                                                                           Pred.
17; }
                                                                                                                  Score
                                                                                                                                                               TNFR-CYS
TNFR-CYS
                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                  TNFR-CYS
                                                                                                                                                                                                            4 X TNFR-CYS.
                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                               EXTRACELLULAR
                                                                                                                                                                                                                                                            OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                        C06465136B16E821 CRC64;
                                                                                           Mismatches
                                                                                                   165;
No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen of activated CI to nerve growth factor
                                                                                                                                                               4
                                                                                         DB 1; Le
3.94e-12;
ches 32;
                                                                                                                                                                        (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                               Length 271;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4 positive or receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                           ω
•-
                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                           Gaps
                                             117
                                                                    93
                                                                                           Ψ
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AC DT

OX40\_MOUSE P47741; 01-FEB-1996

(Rel. 33, Created)

STANDARD;

PRT;

272

B

RESULT

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δ
                                                                                                    В
Qγ
                                   Вþ
                                                                                                                                    Query Match
Best Local Similarity
Matches 33; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J., Claassen E., Noelle R.J., Fell H.; Claassen E., Noelle R.J., Fell H.; "Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions."; J. Immunol. 151:5261-5271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 0X401 RECEPTOR PRECURSOR (OX40 ANTIGEN). TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       ISSP; Y437-4,
MGD; MGT:104512; TXGFL.
PFAM; PF00020; TMFR_C6; 3.
PROSITE; PS00652; TMFR_NGFR_1; 3.
PROSITE; PS50050; TMFR_NGFR_2; 2.
***tqen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUR. J. Immunol. 25:926-930(1995).

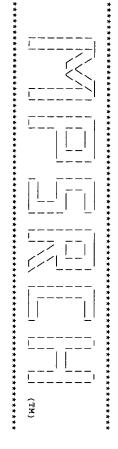
-i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/C
                                                                                                                                                                                                                        CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 221674; CAA79772.1; -.
EMBL; X85214; CAA59476.1; -.
HSSP; P25942; ICDF.
MGD; MGI:104512; TXGP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 95255413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94044750.
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                               MAIN
                                     61
 82 LYCPOTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKPG 131
                                                                   22 VPQALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTC 81
                                                                                                5 VQQPTALLLL-ALTLGVT-ARRLNCVKHTYPS-GHKCCRECQPGHGMVSRC-DHTRDTLC 60
                                   HPC-ETGFYN-EAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPG 108
                                                                                                                                     5.1%;
larity 30.0%;
Conservative
                                                                                                                                                                                                             30153
                                                                                                                                                                                                             MW.
                                                                                                                                     Score 167; DB 1;
Pred. No. 3.84e-12;
22; Mismatches 49
                                                                                                                                                                                                                                                        TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                               TNFR-CYS
                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                               OX40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                             4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                           -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van den Eertwegh A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                           49; Indels
                                                                                                                                                                         Length 272;
                                                                                                                                           6;
                                                                                                                                           Gaps
                                                                                                                                             9
```

Search completed: Tue Jul 25 22:20:18 2000

Job time : 18 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:22:48 2000; MasPar time 14.90 Seconds 867.424 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-09-314-889-4 (1-417) from US09314889.pep 3198 1 MEQRPRGCAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP 417

Scoring table:

PAM 150 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 48.727; Variance 83.543; scale 0.583

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

				,
20 22 23	14 15 16 17 18	10 11 12 13	87654	Result No. 1 2
161 157 157	168 165 164 160 159	204 190 182 179 174	398 383 278 213 211	Score 3198 407 399
4 4 4 5 0 0 0 0 0		5.6 5.4	12.4 12.0 8.7 6.7	Query Match 100.0 12.7 12.5
474 250 415	461 271 325 325 272 277 435	327 335 326 349 260	461 461 332 323 323	Length 417 455
				1
TNR2_MOUSE CD27_MOUSE TNRC_MOUSE	TNR2_HUMAN OX40_RAT VT2_SFVKA OX40_MOUSE CD40_HUMAN TNRC_HUMAN	FASA_MOUSE FASA_HUMAN VT2_MYXVL VC22_VARV CD27_HUMAN	TNR1_PIG TNR1_RAT FASA_PIG FASA_BOVIN FASA_RAT	ID WSL1_HUMAN TNR1_HUMAN TNR1_MOUSE
TUMOR NECROSIS FACTOR CD27L RECEPTOR PRECURS LYMPHOTOXIN-BETA RECEP	NECROSIS RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOXIN-BE	FASL RECEPTOR PRECURSO FASL RECEPTOR PRECURSO TUMOR NECROSIS FACTOR PROTEIN C22/B28 HOMOLO CD27L RECEPTOR PRECURS	NECROSIS NECROSIS RECEPTOR P RECEPTOR P	Description WSL-1 PROTEIN PRECURSO TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR
5.58e-11 2.91e-10 2.91e-10		4.35e-19 2.22e-16 7.37e-15 2.70e-14 2.32e-13	2.50e-60 5.52e-57 3.52e-34 7.37e-21 1.83e-20	Pred. No. 0.00e+00 2.42e-62

4.	4 4	4 4	41	40	39	38	37	36	ω 5	34	<b>ω</b> ω	32	31	30	29	28	27	26	25	24
107	109	108	108	108	109	110	110	108	108	112	111	111	114	116	114	124	131	134	139	146
		ωω •	3.4					3. <b>4</b>				3.5		3.6	3.6	3.9	4.1	4.2	4.3	4.6
883	3707	1245	647	612	400	289	269	103	103	1609	1607	655	1247	799	277	3635	425	671	427	416
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PGCB_MOUSE	DORM MODE	NIDO_MOUSE	GAG_SFV1	OCTC_RAT	LMB_HIRME	CD40_MOUSE	CD40_BOVIN	VA53_VACCV	VA53_VACCC	LMG1_HUMAN	LMG1_MOUSE	ITB5_PAPCY	NIDO_HUMAN	ITB5_HUMAN	OX40_HUMAN	LMA5_MOUSE	NGFR_RAT	RIP_HUMAN	NGFR_HUMAN	NGFR_CHICK
	BASEMENT MEMBRANE-SOFO	NIDOGEN PRECURSOR (ENT	GAG POLYPROTEIN (CORE	PEROXISOMAL CARNITINE	LAMININ B-CHAIN (FRAGM	CD40L RECEPTOR PRECURS	CD40L RECEPTOR PRECURS	PROTEIN A53.	PROTEIN A53.	LAMININ GAMMA-1 CHAIN	LAMININ GAMMA-1 CHAIN	INTEGRIN BETA-5 (FRAGM	NIDOGEN PRECURSOR (ENT	INTEGRIN BETA-5 PRECUR	OX40L RECEPTOR PRECURS	LAMININ ALPHA-5 CHAIN	LOW-AFFINITY NERVE GRO	SERINE/THREONINE PROTE	LOW-AFFINITY NERVE GRO	LOW-AFFINITY NERVE GRO
4.51e-02	2.316-02	3.23e-02	3.23e-02	3.23e-02	2.31e-02	1.64e-02	1.64e-02	3.23e-02	3.23e-02	8.28e-03	1.17e-02	1.17e-02	4.14e-03	2.06e-03	4.14e-03	1.16e-04	8.53e-06	2.73e-06	3.96e-07	2.51e-08

## ALIGNMENTS

Ī	
[5]	
Curr. Biol. 6:1669-1676(1996).	
s a death domain and activates apopt	
RT "Apo-3, a new member of the tumor necrosis factor receptor family,	
Goddard A.D., Bauer K.D., Ashkenazi A.;	
RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,	
MEDLINE;	
RC TISSUE=HEART;	
RN [4]	
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.	
RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;	
[3]	
Science	
related to TNFR-1 and CD95.";	
"Signal transduction by DR3, a death domain	
Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;	
[2]	
Nature 384:372-375(1996).	
"A death-doma	
Grinham C.J., Brown R., Farrow S.N.;	
TISSUE=LYMPHOID;	
Primates; Catarrhini; Hominidae;	
Eukaı	
Homo sapiens (Human).	
(APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYT	
MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PF	
WSL-1 PROTEI	
15-FEB-2000 (Rel. 39, Last	
01-NOV-1997 (Rel. 35,	
DT 01-NOV-1997 (Rel35, Created)	
Q99830;	
Q93038; Q93036; Q93037; Q92983; P78515;	
ID WSL1_HUMAN STANDARD; PRT; 417 AA.	
RESULT 1	

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THEFT TO SEE THE PROPERTY OF SOCION SOCION SOCIETY OF SEE THE PROPERTY OF SOCION SOCIETY OF SEE THE PROPERTY OF SOCION SOCIETY OF SEE THE PROPERTY OF SOCION SOCIETY OF SOCIETY 
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-: FUNCTION: INDICES APOPTOSIS AND ATTIVATES NUCLEAR FACTOR KAPPA-B
-: FUNCTION: DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.

-: SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
THE THERI-ASSOCIATED MOLECULE TRADD AND THE TURFI RECEPTOR TO
ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
NF-KAPPA B SIGNALING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., Fr
Browning J.L., Macdonald H.R., Tschopp J.,
"TRAMP, a novel apoptosis-mediating receptor with sequence
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as low-modified and this statement is not remove entities requires a license agreement (S) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "LARD: a new lymphoid-specific death domain contaregulated by alternative pre-mRNA splicing."; proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97272273.
Screaton G.R., Xu
McMichael A.J., Be
                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
Chaudhary P.M., Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN, AND FETAL LUNG; MEDLINE; 97205335.
  DOMAIN
DOMAIN
                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 4-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunity 6:79-88(1997).
                                                                DOMAIN
                                                                                                            SIGNAL
                                                                                                                               Repeat
                                                                                                                                                        Receptor;
                                                                                                                                                                                                                      PROSITE;
                                           TRANSMEM
                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).

ALTERNATIVE PRODUCTS: THREE ISOFORMS: WSL-1/LARD-1A (SHOWN HERE),

MSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND

LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,

COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.

PTM: GLYCOSYLATED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
PTM: GLYCOSYLATED (PROBABLE).
SIMILARITY: CONTAINS A LA-NGFR/THFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                    U72763 AAC50819.1;
U83599 AAB41434.1;
U83509 AAB41435.1;
U85600 AAB41935.1;
U78029 AAB40918.1;
U74611 AAB39714.1;
U94501 AAC51306.1;
U94504 AAC51309.1;
                                                                                                                                                                                                                                                                                         603366
                                                                                                                                                                                                                                                                                                                U83597;
P19438;
                                                                                                                                                                                                                                                                                                                                                          U75380;
U75381;
                                                                                                                                                                                                                                                PF00020; TNFR_c6; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y09392; CAA70561.1;
Y09392; CAA70559.1;
Y09392; CAA70560.1;
                                                                                                                                                                               PS50050;
                                                                                                                                                                                                                      PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 7-417 FROM N.A.
                                                                                                                                                        Apoptosis;
    1
25
25
200
200
223
                                                                                                                                                                                                                                                                                                                                                          AAC51192.
AAC51193.
                                                                                                                                                                                                                                                                                                                                       AAB41432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu X.-N., Ol
Bell J.I.;
                                                                                                                                                                             TNFR_NGFR_1; 2.
TNFR_NGFR_2; 1.
DEATH_DOMAIN; 1
    24
417
199
220
417
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.E.
                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olsen A.L.,
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

WSL-1 PROTEIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is not removed.
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                                                                                                                                                          Transmembrane;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS
BINDING PROTEIN 1) (TB9I) (P60) (TNF-R1) (P55) (CD120A).
TNFRSF1A OR TNFAR.
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MISSING (IN ISOFORM WSL-S2)
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MEALTPPPATHLS -> SRWCAGNARGRTGMDRGEAGEEGG
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MISSING (IN ISOFORM WSL-S1).
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Banner D.W., D'Arcy A., Janes W., Gentz
Broger C., Loetscher H., Lesslauer W.;
"Crystal structure of the soluble human
beta complex: implications for TNF recep
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tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
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Gray P.W.
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"Two tumor necrosis factor-binding proteins
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EMBO J. 9:3269-3278(1990).
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"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of the human TNF receptor 1 (p60) localization to chromosome 12p13."; Genomics 13:219-224(1992).
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Tabuchi H., Lesslauer W.;
"Molecular cloning and expression
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                                               X-RAY CRYSTALLOGRAPHY (1.85
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Molecular cloning and expression of human and rat tumor necrosis
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61:351-359(1990).
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"Structures of the extracellular domain of the type I tumor necrosis at Structure 4:1251-1262(1996).

C. -i- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF THE ACID SPLINGOMIYELINASE.

C. -I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TWF1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS TO THE EXTRACELLULAR DOMAIN OF TWF1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS TO THE EXTRACELLULAR DOMAIN OF TWF1 COMPLEX OF THE DAMAIN OF TRADD. VARIOUS TRADD. THE RECRUITED TO THE THE DEATH DOMAIN OF TRADD. TO THE TRADD TO THE DEATH DOMAIN OF TRADD. THE RECRUITED TO THE THE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NE-KAPPA B SIGNALING.

-I- SUBSCLLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBSCLLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SUBSCLLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBSCLLULAR LOCATION: THE NEARS ASSESSED THE RECRUITED TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.

-I- SINILARITY: CONTAINS A LA-NGFR/TMFR-TYPE CYSTEINE-RICH REGION.

-I- SINILARITY: CONTAINS A LA-NGFR/TMFR-TYPE CYSTEINE-RICH REGION.
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entities requires a or send an email to modified and this statement is not removed. use by non-profit institutions as long This between SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN an email to license@isb-sib.ch). license agreement (See http://www.isb-sib.ch/announce/ There are no restrictions ng as its content is in Usage Ьy and EMBL a collaboration tor outstation on no

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm"

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PIR; A38208;
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                                                                                                                              Receptor;
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M33294; AAA03210.1;

M58286; AAA36753.1;

M63121; AAA36754.1;

M75866; AAA61201.1;

M75864; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;

M75865; AAA61201.1;
                                                                                                                                                                                                                                              A34899;
                                                                                                                                                                 PF00020; TNFR_c6; PF00531; death; 1.
                                                                                                                                       PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2; PS50017; DEATH_DOMAIN;
                                                                                                                             Transmembrane;
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07-DEC-95.
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GQHUT1.
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TNFR-CYS 2.
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TUMOR NECROSIS |
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TNFR-CYS
N-SMASE A
         DEATH DOMAIN
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                 ACTIVATION DOMAIN (NSD)
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Best Local
 Wong G.H.
"Cloning
necrosis
                                          SEQUENCE;
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CARBOHYD
CARBOHYD
                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P
                                                                                                                                                              TNR1_MOUSE P25118;
                                                                                              Mus musculus (Mouse)
                                                                                                         TNFRSF1A OR TNFR1 OR TNFR-1.
                                 Lewis
                                                                          Mammalia;
                                                                                     Eukaryota;
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                      G.H.,
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                                                                                                                                                                                                                                                         TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVED
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        M., Tartaglia L.A., Lee A., I
G.H., Chen E.Y., Goeddel D.V.,
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Pred. No. 2.42e-62;
81; Mismatches 177
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EMBL; M60468; REMBL; M59377; CMBL; X59238; CEMBL; X57796; CEMBL; L26349; REMBL; M76656; REMBL; M88067; REMBL; M76655; REMBL; M
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HOOI. IMMUDOI. 30:165-175(1993).

HOOI. IMMUDOI. 30:165-175(1993).

HE CHUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING RECRUITS CASPASE-8 TO THE ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPATATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD. ARE RECRUITED TO THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. THIS COMPLEX OF THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KARPA B SIGNALING (BY SIMILARITY).

HOMOTRIMERIZATION: TYPE I MEMBRANE PROTEIN.

HOMOTRIMERIZATION: TYPE I MEMBRANE PROTEIN.
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Mol. Immunol. 30:165-175(1993).
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"Nucleotide sequence of t
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AAA40464.1;
CAA41922 1;
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AAA59361.1;
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function of the murine tumor
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Best Local
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REPEAT
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00020; TNFR_c6; PFAM; PF00531; death; 1
  368
                     392
                                                                                                                         197
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S19021;
                                                                                                                                   LPLVILLGLCLLSEIFISLMCRYPRWRPEVYSIICRDPVP-VKEEKAGK-PLTPAPSPAF::::||::||::||:::|
                                                                                           SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                                      WRQMFWVQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                               CGALHRHTRLLC-SR---RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG
                                                                                                                                                                                 CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL
                                                                                                                                                                                                                                                RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
IGR-FRDQQYEMLKRWRQQQP--AG-LGAVYAALERMGLDGCVEDLRSRLQRGP
                    NGRCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENTLEAL-RNP
                                                          SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                                               SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                                                                                                                      ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQPCLD
                                                                                                                                                                                                                           QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP
                                                                                                                                                                                                                                                                   RDSLCP-QGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:1314884; TNFRSF1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P19438;
                                                                                                                                                                                                                                                                                         119;
                                                                                                                                                                                                                                                                                        h 12.5%;
Similarity 28.7%;
119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 3. PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                     356
44
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84
102
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168
182
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S19021.
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                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       50129
                                        -PAMMLQPG-PQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                 W.
                                                                                                                                                                                                                                                                                                 Score 399; 1
                                                                                                                                                                                                                                                                                        Pred.
79; M
                                                                                                                                                                                                                                                                                                                                                            N-SMASE ACTIVATION D
DEATH DOMAIN.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                POTENTIAL.

R -> G (IN REF. 6)

0710C2E8C3C2B6D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS
                                                                                                                                                                                                                                                                                        No. 1.49e-60;
Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Signal; Apoptosis.
                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FACTOR RECEPTOR 1.
                                                                                                                                                                                                                                                                                                             Length 454;
                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN (NSD)
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                        Gaps
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RESULT
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P50555;
01-OCT-1996
01-OCT-1996
 DOMAIN
DISULFID
                                                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                       Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE SUBSEQUENT CASCADE OF CASPASES (BY SIMILARITY).

-i- SUBUTIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TWERI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO TWERI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NE-KAPPA B SIGNALING (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                     modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
15-JUL-1999 (Rel. 38,
                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                  PROSITE; PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                            entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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Suter B., Pauli U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFRSF1A OR TNFR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                  send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163:263-266(1995).
                                                                                                                                                                                                                                                                                                               U19994; AAC48499.1;
P19438; 1TNR.
                                                                                                                                                                                                                                                                                        PF00020; TNFR_c6; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       PS50050; TNFR_NGFR_2; 2 PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                             Transmembrane;
  22
22
211
234
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126
167
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444
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1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA
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1195
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1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
RECEPTOR 1 PRECURSOR (P
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                             Glycoprotein;
DEATH DOMAIN.
BY SIMILARITY
                                                                                                                                                 CYTOPLASMIC (
4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                            TNFR-CYS
                                                                                                                   N-SMASE
                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                     TUMOR NECROSIS
                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                 ACTIVATION
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                                                                                                                                                                                                                                           Repeat;
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                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                       FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis
                                                                                                                                                                                                                                           Signal; Apoptosis
                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
A Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
T Molecular cloning and expression of human and rat tumor necrosis
T factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein.";
LONA Cell Biol. 9:705-715(1990).
C -!- FUNCTION: RECEPTOR FOR THE ACTIVATED RECEPTOR. THE RESULTING
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION WHICH INITIATES THE
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
C SUBSEQUENT CASCADE OF CASPASES (BY SIMILARITY).
C -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  TNR1_RAT P22934;
                                                                                                                                                                                                                                                                    01-AUG 1991 (Rel. 19, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P
                                                                                                                                                                                                                                                                 TNFRSF1A OR TNFR1 OR TNFR-1.
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                      407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 HPGDREKRESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTAS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQR-WKPKLYSIICGKSTPVKEGEPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRRLGLSEHEIERLELQNGRCLREAQYSMLAEWRRRTSRREATLELLGSVLRDMDLLGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVTWSWDQLP-SRALGPAAAPTL--SPESPAGSPAMMLQPGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-TPP---PATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTP---GYPETQEALCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATAPSFGPITTFSPIPSFSPTTTFSPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNC-SLCPNGTVQLPCLEKQDTICN-CHSGFFLRDKECVSCVNCKNADCKNLCPATSETR
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                                                                                                                                                                                                                                                                                                                                                                                                      EDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                                                                              EDIEEAL-RGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMFW---VQVLLA-----GLVVPLLLGATLTYTYRHCWPHK--PLV----TA-DEAGMEA
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                                                                                                                                                                                                FROM
                                                                                                                                                                                91090841.
                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
182
185
54
86
145
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%;
larity 32.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                STANDARD;
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190
194
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86
145
151
50696
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 398;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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CD72361EC60C9D43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                461
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.50e-60;
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                                                                                                                                                                                                                                                                              (P60) (TNF-R1) (P55).
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                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                          Murinae;
     TNFR1 LEADS
                                                                                                                                                                                                                           Rattus
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REPEAT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M63122; AAA42256.1; PIR; B36555; B36555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00020; TNFR_c6; PFAM; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
   140
                        154
                                              84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL WOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY MITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO TWEFT COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AN NE-KAPPA B SIGNALING (BY SIMILARITY).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                              GDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through
   PCLDCGALHRHTRLLCSRRDTDCGT-CLP-GFYEHGDGCVS-C-PTSTLGSCPERCAAVC
                        VTIPCKE-KONTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAV
                                              HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC - - QVS - QCVSSSP - FYCQ
                                                                    H-VRQCLSCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGT 153
                                                                                          GTRSPRCD-CA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 3. PS50017; DEATH_DOMAIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                 461 AA;
                                                                                                                                                                                                                                                                                  212
235
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                                                                                                                                      Conservative
                                                                                                                                                                                                     12.0%;
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POTENTIAL
                                                                                                                                                                                 ₩,
                                                                                                                                    Score 383;
Pred. No. 5.
73; Mismatc
                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                             POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                X TNFR-CYS.
                                                                                                                                                                                 EB23C05450FBD202 CRC64;
                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                          ACTIVATION DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Signal; Apoptosis
                                                                                                                                                DB 1;
.52e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTOR RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                           Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                      Indels
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REPEAT
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DOMAIN
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                                                                                                Apoptosis;
SIGNAL
                                                                                                                               PROSITE;
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                                                                                                                                                      PFAM; PF00531;
                                                                                                                                                                          EMBL; AJ001202; CAA04596.1;
                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                              myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FASI RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FASA_PIG
                                  REPEAT
                                                                 TRANSMEM
                                                                           DOMAIN
                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartling B., Hoffmann J., Holtz J.,
"Expression of apoptosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APO-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                             RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PEFFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY). SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FAD AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL.
                                                                                                                                                                                                                                                                                                                                                                                                         ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
                                                                                                                                                                                                                                                    SWISS	ext{-}PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWRQMEWVQV-LLAGLVVPLL--LGATLTYTYRH-CWPHKPLVTADEAGM--EALTPPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAFSPNPGFNPTLGFSTTPRFSHPVSSTPISPVFGPSNWHNFVPPVREVVPTQ-G-A-DP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           В.,
                                                                                                                  PS00652; TNFR_NGFR_1; 2.
PS50050; TNFR_NGFR_2; 2.
PS50017; DEATH_DOMAIN; 1.
                                                                                                          Receptor;
                                                                                                                                                     death;
                                                                                                                                                                 TNFR_c6;
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 c; G1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                         lycoprotein;
CYTOPLASMIC (
3 X TNFR-CYS.1.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
DEATH DOMAIN.
                                                                                       FASL RECEPTOR
                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
actyla; Suina; Suidae;
                                                                           EXTRACELLULAR
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                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schulz R., Heusch G., Darmer D.; genes in hibernating and stunned
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                                                      (POTENTIAL)
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                                                                           (POTENTIAL)
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                                                                                                          Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi, Sus.
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                                                                                                          Signal
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Matches 4
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CARBOHYD
                                                                                                                                                                                                                                             PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U1-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                              Apoptosis,
SIGNAL
                                                                                                                                                                                                                                                                                                HSSP; P25445; 1DDF.
PFAM; PF00020; TNFR_c6;
PFAM; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FASA_BOVIN P51867;
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                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U34794; AAC48546.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96226401.
Yoo J., Stone R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 QACD-EQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC
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PS50017;
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; INFR_NGER_2; 2.
; DEATH_DOMAIN; 1.
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. 34, Last sequence as the sequence of the sequ
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38.2%;
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Pred. No. 3.52e-34,
21; Mismatches 38
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                                                                               POTENTIAL
                                                                                                           EXTRACELLULAR
                                                                                                                                     FASL RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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CYTOPLASMIC (POTENTIAL) 3 X TNFR-CYS. TNFR-CYS 1.

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                                                                                                                                                                                                                                                                                                         BIOCHEM. BIOPHYS. Res. COMMUN. 198:666-674(1994).

C. -- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE PROPERTION. RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC STIGNATION. ACTIVE CASPASE-8 INITIATES SHEED SUBSTITUTING CASTASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS ANY HAVE A ROLE IN THE APOPTOSIS. FAS-MEDIATED APOPTOSIS ANY HAVE A ROLE IN THE SUBSCENCE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

C. INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTICEN-STIMULATED SUBCELJULAR LOCATION: TYPE I MEMBRANE PROTEIN.

--- SUBCELJULAR LOCATION: TYPE I MEMBRANE PROTEIN.

--- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q63199;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING (APO-1 ANTIGEN) (CD95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APT1 OR FAS
              TRANSMEM
DOMAIN
                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                              prosite; ps00652; TNFR_NGFR_1; 2.
prosite; ps50050; TNFR_NGFR_2; 2.
prosite; ps50017; Death_Domain; 1.
                                                                                                                                                       PFAM;
                                                                                                                                                         EMBL; D26112; BAA05108.1; PFAM; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                          modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the rat liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                          CHAIN
                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'A variant mRNA species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ONCTRTRNTKCRCKSNFF--CNSSPCEHCNP--CTTC-EHGIIEK 153
                                          DOMAIN
                                                                      SIGNAL
                                                                                   Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 FCCQPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTD-KSHHSDKCIRCSICDEEHGLEVE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHR 149
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                                                                                                                                         PF00020; TNFR_c6; PF00531; death; 1
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto M.,
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llarity 29.5%;
Conservative
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                                                                                    Glycoprotein;
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  POTENTIAL.
CYTOPLASMIC (POTENTIAL)
3 X TNFR-CYS.
                                          FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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                                                                      BY SIMILARITY.
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                                                                                      Transmembrane; Repeat;
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REPEAT
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01-MAY-1992 (Rel. 22,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FASA_MOUSE P25446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe-Fukunaga R.,
Copeland N.G., Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FASL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                    mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi M., Watanabe-Fukunaga R., Nagata S.; "Aberrant transcription caused by the insertion transposable element in an intron of the Fas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APO-1 ANTIGEN) (CD95).
                                                                                                                                                                                                                                antigen that mediates apoptosis.";
Nature 356:314-317(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The cDNA structure, expression,
                                                                                                                                                                                                                                                                                                       Nagata S.;
                                                                                                                                                                                                                                                                                                                         Watanabe-Fukunaga R.,
                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                               "Lymphoproliferation disorder in mice explained by
                                                                                                                                                                                                                                                                                                                                                                        VARIANT LPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 CTR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 CAFCDEGHGLEVE-TNCTRTQNTKCRCKENFY--CNASCC-DHC-YHCTSCGLE-DILEP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 NCSEGLYQ-VGPFCCQPCQPGERKVKD-CTTSGGAPTCHPCTEGEEYTDR-KHYSDKCRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 CQACDE-QASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC-LDCGALHR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 DCAGDFHKKIGLFCCRGCPAG-HYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECAR
                 FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 PROTEDLYTIC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEDLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS. MEDIATED APOPTOSIS. FAS. MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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    TISSUE SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen.";
l. 148:1274-1279(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rel. 35, Last annotation update)
PRECURSOR (APOPTOSIS-MEDIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ıga R., Brannan C.I., Itoh N.,
Jenkins N.A., Nagata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
132
36835
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163
303
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30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                             Brannan C.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
        DETECTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 211; DB 1;
pred. No. 1.83e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH DOMAIN.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  90:1756-1760(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D25D583C909D9D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and chromosomal assignment
                                                                                                                                                                                                                                                                                                                                Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Indels 13;
        TISSUES INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SURFACE ANTIGEN FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of an
                                                                                                                                                                                                                                                                                          defects in Fas
                                                                                                                                                                                                                                                                                                                                  Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of lpr
                                                                                                                                                                                                                                                                                                                                  N.A.,
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RRN OCC OCC DE TO
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                                               SULT 1.

FASA_HUMAN 51....

FASA_HUMAN 51....

9 P25445;

T 01-MAY-1992 (Rel. 22, Created)

JT 01-MAY-1992 (Rel. 22, Last sequence update)

JT 01-MAY-1997 (Rel. 35, Last annotation update)

DT 01-NOV-1997 (REL. 35, Last annotation update)

FASI_RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SUPPASIS ANTIGEN).
                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2; PROSITE; PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A. MEDLINE; 91309137
                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis;
                                                                                                                                                                                                                              101
                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                     34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIVER, LUNG, HEART, AND ADULT OVARY.

DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRODUCTION.
                                                                                                                                                                                                                           TLCDEEHGLEVETNCTLTQNTKCKCKPDFYCDSPGCEHCVRCAS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:95484; FAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A46484; A46484.
; P25445; 1DDF.
                                                                                                                                                                                                      QACDEQASQVALENCSAVADTRCGCKPGWFVECQVS-QCVSSSP 135
                                                                                                                                                                                                                                                    DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDT-FLAWENHHNSECARC
                                                                                                                                                                                                                                                                          NCSEGLYQG-GPFCCQPCQPGKKKVEDCKMNGGTPTCAPCTEGKEYMD-KNHYADKCRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M83649; AAA37593.1;
S56490; AAB25700.1;
S56485; AAB25700.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00020; TNFR_c6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S56486; AAB25700.1;
                                                                                                                                                                                                                                                                                                                Similarity
                                   Eutheria;
                                              Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                     ÅĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 death; 1
                                                                                                                                                                                                                                                                                                                                                                                       21
327
169
186
186
327
162
79
123
162
306
                                                                                                                                                                                                                                                                                                                6.48;
27.98;
                                   Primates;
                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                     37418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                     X.
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                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (P
3 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                            Score 204; DB 1;
Pred. No. 4.35e-19;
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FASL RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                 Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2
                                                                                                                                                                                                                                                                                                                                                  F6BFFC5ACE356EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                -> N (IN LPR)
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                             SURFACE
                                                                                                                                                                                                                                                                                                                          Length 327,
                                                                                                                                                                                                                                                                                                    Indels
                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ьy
                                                                                             ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
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                                                                                                                                                                                                                                                                                                    4.
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DOMAIN
CARBOHYD
CARBOHYD
                                                                 REPEAT
REPEAT
                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                             EMBL; M67454; AAA63174.1; EMBL; X63717; CAA45250.1; PIR; A40036; A40036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IT FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC CASTALED ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH.

SUICIDE OF MATURE T-CELLS, OR BOTH.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

SINILARITY: CONTAINS A LA-NGFR/TWER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 384:638-641(1996)
SEQUENCE
                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oehm A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                     REPEAT
                                                                                                           DOMAIN
                                                                                                                      TRANSMEM
                                                                                                                                    DOMAIN
                                                                                                                                                 CHAIN
                                                                                                                                                                                       Apoptosis;
                                                                                                                                                                                                    PROSITE; PS50050; PROSITE; PS50017;
                                                                                                                                                                                                                            PROSITE; PS00652;
                                                                                                                                                                                                                                             PFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.; "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 97122332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 218-335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krammer P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li-Weber M., Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sameshima M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Itoh N., Yonehara S., Ishii
                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The polypeptide encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can mediate apoptosis.";
1 66:233-243(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm"
                                                                                                                                                                                                                                                                                                  S24543;
                                                                                                                                                                                                                                                                                   1DDF; 12-NOV-97.
                                                                                                                                                                                                                                            PF00020; TNFR_c6; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Behrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92268122
                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                  S24543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hase A.,
ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267:10709-10715(1992).
                                                                                                                                                                                                    TNFR_NGFR_2;
DEATH_DOMAIN;
                                                                                                                                                                                                                              TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ι.,
                         16
335
173
190
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166
166
183
127
166
314
                                                                                                                                                                                      Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Falk W.,
S., Dheir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the tumor necrosis factor/nerve growth fac
Sequence identity with the Fas antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seto
Æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dhein J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Υ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the cDNA for human cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cloning of the APO-1 cell surface
                                                  TNFR-CYS
TNFR-CYS
                         DEATH DOMAIN POTENTIAL.
                                                                                          CYTOPLASMIC (POTENTIAL)
3 X TNFR-CYS.
                                                                                                                                  FASL RECEPTOR EXTRACELLULAR
0139942535111410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pawlita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yonehara M., Mizushima S.I., Nagata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ita M.,
Trauth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226-240;
                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor/nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maier
B.C.,
                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269-291
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Query Match

Score 190;

DB

Length 335;

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OF PERFERENCE OF STREET STREET
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                                           DЬ
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Matches
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                                                                                                                                Query Match
                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 91335768. Upton C., Macen J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VT2_MYXVL
                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 184:370-382(1991).
-!- FUNCTION: BINDS TO THE ALPHA AND BETA. PROBABLY ERBACH CELLULAR TARGET AND THEREBY DEAMPENING THE ANTIVIRAL EFFECTS OF THE CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A40566; GQVZML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M95181; AAA46632.1; -. EMBL; A23729; CAA01688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leporipoxvirus.
                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myxoma virus expresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
    14
                                                                                                           Local
                                                J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVALENCSAVADTRCGCKPGWFVECQVS-QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVEI-NCTRTQNTKCRCKPNFFCNSTVCEHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQFCHKPCPPGE-RKARDCTVNGDEPDCVPCQEGKEYTD-KAHFSSKCRRCRLCDEGHGL 113
                                TLLLAYVACVYGGGAPYGADRGKCRGNDYEKDGL-CCTSCPPGSYASRLCG-PGSDTVCS 62
    ALLLYLLGARAQGGTR-SP-RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P19438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00020; TNFR_c6;
                                                                                       h 5.7%;
Similarity 30.9%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pean Bioinformatics Institute. The non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
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                                                                                                                                                                     326
186
186
104
1147
1146
166
181
205
238
35208
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38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR_NGFR_1; 2.
TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR_NGFR_1;
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Last annotation update)
SOLUBLE RECEPTOR PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Signal.
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                                                                                       Score 182; DB 1;
Pred. No. 7.37e-15;
23; Mismatches 45
                                                                                                                                                                                                                                                                                          TNFR-CYS
                                                                                                                                                                                                                                                                                                                                   TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS
4 X TNFR-CYS.
                                                                                                                                                                       POTENTIAL.
ABBF027E947292FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      er M., McFadden G.;
reted protein with homology
family that contributes to
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                         45;
                                                                                                                                Length 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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E POTENTIAL
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Best Local
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VC22_VARV
P34015;
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DOMAIN
REPEAT
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                                                                                                                                                            CD27_HUMAN
P26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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RESULT
LID CLI
AC PL
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DT 01
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DT 
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EMBL; X67117; CAA47540.1; -
PIR; D36858; D36858.
PIR; S35987; S35987.
PIR; S46888; S46888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=INDIA-1967
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variola virus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 01-FEB-1994 (Rel. 01-JUN-1994 (Rel.
                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protective mechanisms.";
FEBS Lett. 319:80-83(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shchelkunov S.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00020; TNFR_c6; 2.
PROSITE; PS00652; TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                        Homo sapiens (Human)
                                                                                         TNFRSF7 OR CD27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shchelkunov S.N., Blinov V.M., Genes of variola and vaccinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 IIINGRDAAPYTPPNGKCKDTEY-KRHNL-CCLSCPPGTYASRLC-DSKTNTQCTPCGSG
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  Eutheria;
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                                Metazoa;
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     Primates;
                             Chordata;
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27;
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Pred. No. 2.70e-14;
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TNFR-CYS 1.
TNFR-CYS 2.
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     Catarrhini;
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     Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 349;
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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A46517; A46517.
P; P19438; 1NCF.
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TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.
PTM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).
SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH
DATABASE: NAME-PROW; NOTE-CD guide CD27 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND A ROLE IN SURVIVAL OF ACTIVATED T-CELLS. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encopean Bioinformatics Institute. There are no restrictly py non-profit institutions as long as its content
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                                                                             QDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSS
                                                                                                                    GVSFSP-DHHTRPHCESCRHCN--SGLL-VRNCTITANAECACRNGW--QCRDKECTECD 121
                                                                                                                                                                                            LCVLGTLVGLSATPAPK-SCPERHYWAQGKLCCQMCEPGTFLVKDCDQHRKAAQCDPCIP
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Pred. No. 2
34; Mismat
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EXTRACELULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
3 X TNFR-CYS 1.
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 3.
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PHOSPHORYLATION (POTENTIAL).

A -> T (IN REF. 2).
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RESULT ACCURATE RESULT ACCURAT
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Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King Kohno T., Brewer M.T., Thompson R.C., Vannice J.L.;

Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;

"A second tumor necrosis factor receptor gene product on the second tumor necrosis factor inhibitor.";

naturally occurring tumor necrosis factor inhibitor.";

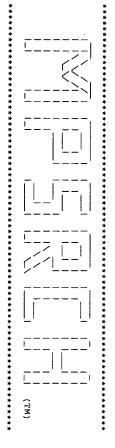
naturally occurring tumor necrosis factor inhibitor.";
                                                                                                                                                                                                          "Purification and partial amino acid sequdistinct tumor necrosis factor receptors J. Biol. Chem. 265:20131-20138(1990).
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15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS
BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) ()
                                                        Characterization of ligand phosphorylation.";
                                                                                           MEDLINE; 93016040.
Pennica D., Lam V.T., Mize Lipari M.T., Goeddel D.V.; "Biochemical properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                            CHARACTERIZATION
                                                                                                                                                                                                                                                                         Loetscher H., Brockhaus M.;
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MEDLINE; 91056048.
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Science 248:1019-1023(1990).
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Eukaryota; Metazoa;
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TNFRSF1B OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                         Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified frourine. Evidence for immunological cross-reactivity with tumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complementary DNA cloning of a receptor for tumor necrosis and demonstration of a shed form of the receptor."; Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ringold G.M.;
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Mammalia; Eutheria; Primates;
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CRYSTALLOGRAPHY (2.3
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90349572.
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ANGSTROMS)
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D.V., Desauvage
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REPEAT
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DOMAIN
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                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                        Phosphorylation;
SIGNAL 1
                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                CHAIN
                                                                                          DISULFID
                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND WYETH-AYERST). USED TO TREAT MODERATE TO SERVERE RHEUMATOID ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LICAND-BINDING PORTION OF TWFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO TWF ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.

SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION. DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR THE ALPHA. HIGH AFFINITY FOR APPROXIMATELY 5-FOLD LOWER AFFINITY FOR THE BETA. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PTM: PHOSPHORYLATED: MAINLY ON SERINE RESIDUES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm" DATABASE: NAME=Enbrel; NOTE=Clinical information on WWW-"http://www.enbrelinfo.com/".
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A36007;
A36475;
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M35857; AAAS3262.1;
U52165; AACS0622.1;
U52156; AACS0622.1;
U52157; AACS0622.1;
U52159; AACS0622.1;
U52159; AACS0622.1;
U52160; AACS0622.1;
U52161; AACS0622.1;
U52162; AACS0622.1;
U52163; AACS0622.1;
U52163; AACS0622.1;
U52164; AAAS9755.1;
M55994; AAAS9755.1;
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TNFR-CYS 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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01-APR-1990 (Rel. 14,
01-OCT-1996 (Rel. 34,
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01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mallett S., Fossum S., Barclay A.N.;
"Characterization of the MRC OX40 antigen of activated CD4 positive lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
TISSUE-T-CELL;
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REPEAT
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PIR; S12783; S12783.
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THER-CYS 4.
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R -> M (IN REF. 1 AND 3).
A -> T (IN REF. 4).
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No. 2.97e-12;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Tue Jul 25 22:24:16 2000; MasPar time 23.31 Seconds 843.833 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-09-314-889-4 (1-417) from US09314889.pep 3198

1 MEQRPRGCAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP 417

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir64 1:pir1 2:pir2 3:pir3 4:pir4

Mean 47.731; Variance 92.974;

scale 0.513

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

112.7 112.5 112.4 112.0 6.4 6.4 5.9 5.9 5.7	455 461 461 461 461 324 314 314 314 360 360	112222212	GOHUT1 GOMST1 JC4302 JF2826 GORTT1 JC2395 A46484 I37383 A40036 GOVZML D36858 A46517	tumor necrosis factor fas antigen precursor apoptosis mediating m FAS soluble protein - apoptosis mediating s T2 protein - myxoma v gene G4R protein - va GD27 antigen precurso	7.65e-55 2.92e-53 4.61e-53 1.68e-50 8.54e-18 1.42e-16 1.42e-14 3.60e-14 3.60e-14 3.60e-14 3.60e-14
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	461	۰			1.73e-11
		۲	A35356	tumor necrosis factor	1.67e-10
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5.1	325	N	B43692	•	7.46e-10
5.0	272	2	148700	gene ox40 protein - m	3.29e-09
	277	Ν	A60771		4.75e-09
5.0	435	Ν	154182		3.29e-09
5.0	474	2	B38634	tumor necrosis factor	2.27e-09
4.9	250	۲	A49053	CD27 antigen precurso	9.90e-09
4.9	459	N	I48854	gene murine tumour ne	9.90e-09
4.8	656	2	149299	receptor interacting	4.25e-08
4.6	416	μ	JN0006	nerve growth factor r	5.24e-07
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## ALIGNMENTS

#cross-references MUID: #accession A34900 #amolecule_type mRNA	rs al	##molecule_type mRNA ##residues_ 1-45 ##cross-references G P ##experimental_sourc part ##note part ##note ##note	#acression A	rs al -ref sion olec esid ross	1 NAMES
#CILLE molecular Clusing and expression of a receptor for number tumor necrosis factor. #cross-references MUID:90235285 #accession A34900 ##molecule_type mRNA	K.J.; Lee, A.; Ricanger, G.A.; Lentz	#molecule_type mRNA   #residues_ 1-455 ##label LOE   #residues_ 1-455 ##label LOE   #cross-references GB:M58266; GB:M33480; NID:g339753; PIDN:AAA36753.1;  #cross-references GB:M58266; GB:M34866; NID:g339753; PIDN:AAA36753.1;  #cross-references GB:M58266; GB:M34866; NID:g339753; PIDN:AAA36753.1;  #cross-references GB:M58266; GB:M34866; NID:g339753; PIDN:AAA36753.1;  #cross-references GB:M58266; PIDN:AAA36753.1;  #cross-references GB:M58266; PIDN:AAA36753.1;  #cross-references GB:M58266; PIDN:AAA36753.1;  #cross-references GB:M58266; PIDN:AAA367553.1;  #cross-references GB:M58266; PIDN:AAA36753.1;  #cross-references GB:M58266; PIDN:AAA367553.1;  #cross-references GB:M58266; PIDN:AAA367553.1	#authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.  #journal Cell (1990) 61:351-359  #title Molecular cloning and expression of the human 55 kd tumor  #cross-references MID:90235284  #accession A34899	#authors Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F. #journal Genomics (1992) 13:219-224 #title Structure of the human TNF receptor 1 (p60) gene (TNRF1) and #cross-references MUID:92250049 #accession A38208 ##molecule_type DNA ##residues_ 1-455 ##label FUC ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748; #DDN:AAA61201.1; PID:g339750	GOHUTI #type complete tumor necrosis factor receptor 1 precursor - human p55 tumor necrosis factor receptor; TNF receptor tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor) #formal_name Homo sapiens #common_name man 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999 A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38258; A60594; A35010; JC2404

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REFERENCE
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein. #cross-references MUID:91017509
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#accession A36555
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##molecule_type DNA
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#accession JT0758
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#accession S12057
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30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
##residues 107-128;162-167,'X',169-201 ##label HI2
107-128;162-167,'X',169-201 ##label HI2
##note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the
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cession C36555
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NCE A36555
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##cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
##note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
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##cross-references GB:M37764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
                                                                                                                   Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.
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R.; Aderka, D.; Holtmann, H.; Wallach, D.
EMBO J. (1990) 9;3269-3278
Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
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                                                                                                                                                                                                    Eur. J. Immunol. (1990) 20:1167-1174
                                                                                                                                                                                                                                                 Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield,
                                                                                                                                                                                                                                                                                  A60231
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                                                                                                                                                                                                                                                                                                            1-13 ##label KEM
                        41-43,'X',45-53,'X',55-57 ##label SEC
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#cross-references MUID:90110215

#accession A35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#cross-references MUID:95128033
#accession JC2404
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127-167
168-196
212-234
235-455
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41-201
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ap_position 12p13.2-12p13.2
itrons 13/3; 65/1; 108/1; 158/1; 184/2;
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This protein is one of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##experimental_source cancer patient serum NCE A60594
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##residues 41-60 ##label GAT
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##residues 41-53,'
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##residues 41-45 ##label ENG
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Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.
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                                                                                                                                                                                                                                                                                                                                                                                                   duplication;
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#length 455
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J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
R.S.; Granger, G.A.
roc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
                                                                                                                    predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain extracellular #status predicted #label EXT\
#product TMF binding protein 1 (tumor necrosis factor
alpha inhibitor) #status experimental #label TBP1\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain NGF receptor repeat homology #label NG4\
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                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 1 #status
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#domain intracellular #status predicted #label INT\
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#molecular-weight 50494
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##molecule_type mRNA
##residues 1-454 ##label LEW
##cross-references GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
-REFERENCE A40254
                                                                                        REFERENCE
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Best Local
                                                                                                                                                           murine receptors for tumor necrosis factor.
#cross-references MUID:91246168
#accession B40254
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#accession A38634
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                                                                  #authors
                                                                                                        ##residues 1-454 ##label GO2
##cross-references GB:M60468; NID:g199825;
                                                                                                                                                  ##molecule_type mRNA
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Local Similarity 29.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEEAL 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is
Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
Eur. J. Immunol. (1991) 21:1649-1656
Cloning, expression and cross-linking analysis of the murine
                                                                                                                                                                                                                                  Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A. Mol. Cell. Biol. (1991) 11:3020-3026
Molecular cloning and expression of the type 1 and type 2
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30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                        S16677
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Pred. No. 7.65e-55;
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                                                                                                        PIDN:AAA39751.1; PID:g199826
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#accession S19021
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                                                                                                                                                                                                                                       144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues 1-454 ##label ROT
##cross-references EMBL:x57796; NID:g54848; PIDN:CAA40936.
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                      SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                             SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                       SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                                                               WRQMFWVQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                                         CGALHRHTRLLC-SR---RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG
                                                                                                                                                                                                                                                                            CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL 214
                                                                                                                                                                                                                                                                                                                                                              QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP 157
                                                                                                                                                                                                                                                                                                                                                                                                          RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
                                                                                                                                                                                                                                                                                                                      ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQPCLD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119;
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Similarity 28.7%;
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   receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenetics (1994) 39:450-451 Nucleotide sequence of the TNF t endothelioma cell line.
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type I receptor
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##residues 1-7 ##label SU2
##experimental_source kidney cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-461 ##label SUT
##cross-references GB:U19994; NID:g1141752; PIDN:AAC48499
PID:g1141753
  244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 PAAAPTLSPESPAGS-PAMMLQPG-PQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVE
                                         261 LATAPSFGPITTFSPIPSFSPTTTFSPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 12.4%;
Local Similarity 32.3%;
                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                               93
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                                                                                                                                                                                                                                                                                                                                                                           33 HPGDREKRESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTAS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | IR-FRDQQYEMLKRWRQQQP--AG-LGAVYAALERMGLDGCVEDLRSRLQRGP 417
  L-TPP---PATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTP---GYPETQEALCP
                                                                                                                                                                                                        LNC-SICPNGTVQLPCLEKQDTICN-CHSGFFLRDKECVSCVNCKNADCKNLCPATSETR 201
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                                                                                QMFW---VQVLLA-----GLVVPLLLGATLTYTYRHCWPHK--PLV----TA-DEAGMEA
                                                                                                                                                                                                                                                                                                                                      QGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGRCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENILEAL-RNP 444
                                                                                                                     NDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRYQR-WKPKLYSIICGKSTPVKEGEPEP 260
                                                                                                                                                                   LDCGALHRH-T-RLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWR
                                                                                                                                                                                                                                                    ENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC 141
                                                                                                                                                                                                                                                                                             ENHL-TQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKN---QYR--KY-WSETLF-Q-C 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC4302 #type complete
tumor necrosis factor receptor p55 precursor - pig
#formal_name Sus scrofa domestica #common_name domestic
29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suter, B.; Pauli, U.
Gene (1995) 163:263-266
Cloning of the cDNA encoding the porcine p55 tumor necrosis
factor receptor.
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JC4302
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#product tumor necrosts factor receptor p55 #status
predicted #label MAT\
#domain extracellular cysteine rich #status predicted
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NGF receptor repeat homology #label NGF\
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Pred. No. 4.61e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                     81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       160;
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Best Local
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#accession I57826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDSLCP-QGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRRLGLSEHEIERLELQNGRCLREAQYSMLAEWRRRTSRREATLELLGSVLRDMDLLGCL 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGAGPILPMPPASTPVPTPLPKWGGSAHSAHSAPAQLADADPATLYAVVDGVPPTRWKEF
                                  NGGCLREAQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGCLENILEAL-RNP 444
                                                                     PAAAPTLSPESPAGS-PAMMLQPG-PQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVE
                                                                                                     SVPAPTSVQKWEDSAHPQRPDNADLAILYAVVDGVPPARWKEFMRFMGLSEHEIERLEMQ
                                                                                                                                          SPLDS-AHTL-LAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV-TWSWDQLPSRALG
                                                                                                                                                                                                               WRQMFWVQV-LLAGLVVPLL-LGATL-TYTYRH-CWPHKPLVTADEAGMEALTPPPATHL
                                                                                                                                                                                                                                 LPLVILLGLCLLSFIFISLMCRYPRWRPEVYSIICRDPVP-VKEEKAGK-PLTPAPSPAF 272
                                                                                                                                                                                                                                                                                  CGALHRHTRLLC-SR---RDTDCGTCLPGFYEHGDGCVS-CPTSTLGSC--PERCAAVCG 196
                                                                                                                                                                                                                                                                                                                                                      ECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQPCLD 143
                                                                                                                                                                                                                                                                                                                                                                                       QCLSCKTCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNGTVTIP 157
                                                                                                                                                                                                                                                                                                                                                                                                                         RSPRCDCAGDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNS
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 IGR-FRDQQYEMLKRWRQQQP--AG-LGAVYAALERMGLDGCVEDLRSRLQRGP
                                                                                                                                                                           SPTSGFNPTLGFSTPGFSSPVSSTP-ISPIFGPSNWHFMPPVSEVVPTQGADPLLYESLC
                                                                                                                                                                                                                                                                                                                 CKETQ-NTVCNCHAGFFLRESECVPC--SHCKKNEECMKLCLPPPLANVTNPQDSGTAVL
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13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 20//3
#superfamily tumor necrosis factor receptor type 1;
#confor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Immunol. (1993) 30:165-176
Genomic organization and promoter function
tumor necrosis factor receptor beta gene
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.0%;
llarity 28.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine receptor
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Pred. No. 1.68e-50;
79; Mismatches 183
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Best Local :
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212-234
235-461
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84-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 12.0%;
Local Similarity 29.8%;
                     LLYGSLNPVPIPAPVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEFMRLLGLSE 389
                                                                                                                                                                                                                                                                                                               VTIPCKE-KQNTVCNCHAGFFLSGNECTPCSHCKKNQECMKLCLPPVANVTNPQDSGTAV
                                                                                                                                PAFSPNPGFNPTLGFSTTPRFSHPVSSTPISPVFGPSNWHNFVPPVREVVPTQ-G-A-DP
                                                                                                                                                                                                                         LLPLVIFLGLCLLFFICISLLCRYPQWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASI
                                                                                                                                                                                                                                                                     PCLDCGALHRHTRLLCSRRDTDCGT-CLP-GFYEHGDGCVS-C-PTSTLGSCPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                     H-VRQCLSCKTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFQCVDCSPCFNGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTRSPRCD-CA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQETVCEVCDKGTFTASQN
LPSRALGPAAAPT-LSP-ESPAGSPAMMLQPG-PQ-LYDVMDAVPARRWKEFVRTLGLRE
                                                                                                                                                                            GWRQMFWVQV-LLAGLVVPLL--LGATLTYTYRH-CWPHKPLVTADEAGM--EALTPPPA
                                                                                                                                                                                                                                                                                                                                                           HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC--QVS-QCVSSSP-FYCQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This protein is one of two known receptors for both TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (cachectin) and TNF-beta (lymphotoxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Himmler, A.; Maurer-Fogy, I.; Kroenke, Pfizenmaier, K.; Lantz, M.; Olsson, I Stratowa, C.; Adolf, G.R. DNA Cell Biol. (1990) 9:705-715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *superfamily tumor necrosis factor receptor receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular cloning and expression of human and rat tumo necrosis factor receptor chain (p60) and its soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor receptor 1 precursor - rat
tumor necrosis factor binding protein 1 (TWF blocking factor)
#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
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#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label NEM\
#domain intracellular #status predicted #label INT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain extracellular #status predicted #label EXT\
#product tumor necrosis factor binding protein #status
predicted #label TBP\
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#product tumor necrosis factor receptor type 1 #status
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Pred. No. 4.15e-50;
73; Mismatches 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461
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44-79
81-124
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#cross-references MUID:92148151
#accession A46484
                                                                                 #journal
                                                                                                                            #authors
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#accession JC2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references DDBJ:D26113; NID:g468488;
##experimental_source liver
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cession PC2246
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                                                                                                                                                                                                                                                                                                                                                                                                                   154 CTR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 CAFCDEGHGLEVE-TNCTRTQNTKCRCKENFY--CNASLC-DHC-YHCTSCGLE-DILEP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCAGDFHKKIGLFCCRGCPAG-HYLKAPCTEPCGNSTCLVCPQ-DTFLAWENHHNSECAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CQACDE-QASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC-LDCGALHR 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%;
Similarity 30.1%;
                                                                                                                                                                                                                                                                                                                                                                            152
                                    Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, Copeland, N.G.; Jenkins, N.A.; Nagata, S. J. Immunol. (1992) 148:1274-1279
The cDNA structure, expression, and chromosomethe mouse Fas antigen.
                                                                                                                                                                                 #formal_name Mus musculus #common_name hou:
18-Jun-1993 #sequence_revision 18-Nov-1994
16-Jul-1999
                                                                                                                                                                                                                                                               A46484 #type complete apoptosis-mediating membrane-associated polypeptide
                                                                                                                                                              A46484; A47254
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20-Feb-1995 #sequence_revision
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Fas antigen precursor - rat
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26; Mismatches
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Pred. No. 8.54e-18;
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20-Feb-1995 #text_change
                                                            and chromosomal assignment
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Matches 2
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81-124
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##cross-references GB.M83349; DID:g193225; PID:g193226
##cross-references GB.M3340; Discrephage cell line
##experimental_source BAM3 macrophage cell line
##experimental_source EAM3 macrophage cell line
##enote sequence extracted from NCBI backbone (NCBIN:81544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TLCDEEHGLEVETNCTLTQNTKCKCKPDFYCDSPGCEHCVRCAS 144
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##cross-references GB:S56490; NID:g298505; PID:g298506
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                                                                                                                                                                                                       ##cross-references EMBL:247993; NID:g728578; PID:g695539
X #length 314 #molecular-weight 35386 #checks
                                                                                                                                                                                                                                                                ##molecule_type mRNA
                 114
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                 EVEI-NCTRTQNTKCRCKPNFFCNSTVCEHC
                                                       GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 100
                                                                                        GQFCHKPCPPGE-RKARDCTVNGDEPDCVPCQEGKEYTD-KAHFSSKCRRCRLCDEGHGL 113
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Similarity 27.9%;
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Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
Aberrant transcription caused by the insertion of an eatransposable element in an intron of the Fas antigen
of lpr mice.
                                                                                                                                                                                                                                                                                                                                                                           Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, J. Immunol. (1995) 154:2706-2713
Three functional soluble forms of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #domain NGF receptor repeat homology #label NGF\
#domain NGF receptor repeat homology #label NG4
#length 327 #molecular-weight 37417 #checksum 8479
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FAS soluble protein - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996
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                                                                                                                                                                                                                                                                                                                                                         nree functional soluble forms of the apoptosis-inducing Fas molecule are
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mRNA
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preliminary
                                                                                                                                                                                                                                               1-314 ##label RES
                                                                                                                                                                                                                                                                                  preliminary; translated
                                                                                                                                                5.9%;
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Pred. No. 1.42e-16;
                                                                                                                                Pred.
                                                                                                                                                  Score 190; DB 2;
Pred. No. 3.60e-14;
                                                                                                                                  Mismatches
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FEATURE
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85-128
174-190
SUMMARY
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##cross references EMBL:X63717; NID:g28741; PID:g28742
REFERENCE A38142
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*cross-references MUID:92268122

*accession A38142
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#pp_position 10q24.1-10q24.1

FFICATION #superfamily NGF receptor repeat homology apoptosis; surface antigen; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary; not compared with conceptual translation ##molecule_type nucleic acid ##residues 1-134,'Q','136-335 ##label OEH
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##residue
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    101
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                                                                             44
                                                                                                     GQFCHKPCPPGE-RKARDCTVNGDEPDCVPCQEGKEYTD-KAHFSSKCRRCRLCDEGHGL 113
    QVALENCSAVADTRCGCKPGWFVECQVS-QC
                                                                             GLFCCRGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 100
                                      EVEI-NCTRTQNTKCRCKPNFFCNSTVCEHC 143
                                                                                                                                                                             5.9%;
Similarity 34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth, B.C.; Ponsting, H.; Krammer, P.H.
J. Biol. Chem. (1992) 267:10709-10715
purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh, N.; Yonehara, S.; Ishii, A.; Yon
S.I.; Sameshima, M.; Hase, A.; Seto,
Cell (1991) 66:233-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis-mediating surface
surface antigen APO-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krammer, P.H.
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17-Jan-1992 #sequence_revision 17-Jan-1992
                                                                                                                                                                                                                                    #domain signal sequence #status predicted #label SIG\
#domain NGF receptor repeat homology #label NG4\
#domain transmembrane #status predicted #label TMM
#length 335 #molecular-weight 37732 #checksum 4899
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                                                                                                                                                        Score 190; DB 2;
Pred. No. 3.60e-14;
18; Mismatches 35
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eto, Y.; Nagata,
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J.; Trauth
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RESULT
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Best Local S
Matches 3
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106-147
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#title
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#accession A40566
                                                                                                                               #description
                                                                                                                                                                                                         #authors
                                                                                                                                                                                                                                                                                                                                                        #description
                                                                                                                                                    #submission
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##experimental_source strain India-1967, isolate
                 ##cross-references EMBL:X67117; NID:g516428; PID:g516449
                                    ##residues
                                                      ##molecule_type DNA
                                                                                                                                                                                                                        ##experimental_source strain India-1967, ssp. major, isolate Ind3
NCE S46868
                                                                                                                                                                                                                                                           ##residues 1-349 ##label BLI#ross-references GB:X69198; NID:g456758; PID:g457087
                                                                                                                                                                                                                                                                                                ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLLAYVACVYGGGAPYGADRGKCRGNDYEKDGL-CCTSCPPGSYASRLCG-PGSDTVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%;
Similarity 30.9%;
                                                                                                          Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.;
S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenii
Shchelkunov, S.N.; Sandakhchiev, L.S.
submitted to the EMBL Data Library, April 1992
Nucleotide sequence analysis of the region of v.
XhoI F O H P Q genome fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily myxoma virus T2 protein; NGF receptor repeat
                                                                                            S46888
                                                                                                                                                                                                                                                                                                                                        D36858
                                                                                                                                                                                                                                                                                                                                                        submitted to GenBank, not shown.
                                                                                                                                                                                                                                                                                                                                                                                             Blinov, V.M
                                                                                                                                                                                                                                                                                                                                                                                                                                 D36858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name variola virus
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene G4R protein - variola virus
B28R protein (COP)
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A40566
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Virology (1991) 184:370-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T2 protein - myxoma virus (strain Lausanne)
#formal_name myxoma virus
31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
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                                    1-349 ##label KOL
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#domain NGF receptor repeat homology #label
#binding_site carbohydrate (Asn) (covalent)
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Pred. No. 8.07e-13;
23; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                           November
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Best Local
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110-151
  #map_position #introns
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#accession A46454
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**Backett (1993) 319:80-83

**#Journal FEBS Lett. (1993) 319:80-83

**#Litle Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.

**Cross-references MUID:93202281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:93094588
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                                                                                                             ##molecule_type mRNA
# residues 1-58,'A',60-260 ##label CAM
# residues 1-58,'A',60-260 ##label CAM
##cross-references GB:M63928; NID:g180084; PIDN:AAA58411.1;
##cross-reference extracted from NCBI backbone (NCBIN)
##note NCBIP:60289)
##cross-references GDB:132582; OMIM:186711

Ap_position 12p13-12p13

Atrons 46/1; 90/1; 150/1; 180/1; 220/1
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                                                                                                A soluble CD27
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Similarity 27.1%;
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                                                                                                                                                                                                                                                       Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B. J. Immunol. (1991) 147:3165-3169

The T cell activation antigen CD27 is a member of the nerve growth factor/tumor necrosis factor receptor gene family.
                                                             GDB:CD27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic organization and human CD27 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loenen, W.A.; Gravestein, L.A.; I
Hagemeijer, A.; Borst, J.
J. Immunol. (1992) 149:3937-3943
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#molecular-weight 38189 #checksum :
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121-188
192-211
212-260
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21-260
21-191
27-63
                                                                                                                                                                                                                             #title A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor. #cross-references_MUID:91045991
                                                                                                                                                                                                                                                                                       #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #type complete
tumor necrosis factor receptor type 2 precursor - human
75K tumor necrosis factor receptor
#formal_name Homo sapiens #common_name man
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
                Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; La
Gentz, R.; Brockhaus, M.; Lesslauer, W.
Cytokine (1990) 2:231-237
Two human TNF receptors have similar extracellular,
                                                                                                                                                                                                                                                                                                         A36475
Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, C.H.; Thompson, R.C.; Vannice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.P.; Jerzy, R.; Dower, S.K.; Cosman, D.; G
Science (1990) 248:1019-1023
A receptor for tumor necrosis factor defines
family of cellular and viral proteins.
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duplication; glycoprotein; homodimer; phosphoprotein;
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  distinct intracellular, domain
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#domain NGF receptor repeat homology #label NG2\
#region proline/serine/threonine-rich\
#domain transmembrane #status predicted #label TMN\
#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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ces GB:M55994; GB:M38549;
PID:g339758
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#domain extracellular #status predicted #label EXT\
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                                                                                                                                                                                                                                                                                       (1990) 87:8331-8335
                                                                                                                                NID: g339757; PIDN: AAA36755.1;
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sequences
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#cross-references MUID:91370690
#accession A48416
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#accession B35010
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##residues 23-461 ##label DEM
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##note sequence extracted from NCBI backbone (NCBIN:63368,
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PID:g825701
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Gene (1994) 150:381-386
Cloning, sequencing and partial functional characterization
of the 5' region of the human p75 tumor necrosis factor
receptor-encoding gene (TNF-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
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J. Biol. Chem. (1990) 265:20131-20138
Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HI60 cells.
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Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
                                                                                                                                                                                                                                                                                                                     the list of introns is incomplete
#superfamily tumor necrosis factor receptor type
receptor repeat homology
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#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain NGF receptor repeat homology #label NG4\
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#accession S12783
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##residues 1-271 ##label
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hes 24; Conservative
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EMBO J. (1990) 9:1063-1068
Characterization of the MRC OX40 antigen of activated CD4
positive T lymphocytes - a molecule related to nerve gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B43692 #type complete
T2 protein - rabbit fibroma virus
#formal_name rabbit fibroma virus, Shope fibroma virus
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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nerve growth factor receptor homolog
#formal_name Rattus norvegicus #common_name Norway rat
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                  Upton, C.; DeLange, A.M.; McFadden, G.
Virology (1987) 160:20-30
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#length 271 #molecular-weight 29895 #checksum 379
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preliminary
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Pred. No. 5.14e-10;
17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 168; DB 1; L, Pred. No. 1.67e-10; 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
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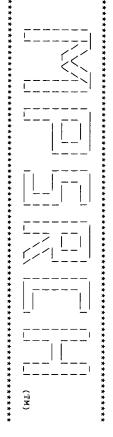
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                   106-147
                                                                                                                                                                                                                                                                                                                                        64 - 105
                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:M17433
##CICATION #superfamily myxoma virus T2 protein; NGF receptor repeat
                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
##residues 1-325 ##label UPT
                                                                      94 A-CDEQASQVALENCSAVADTRCGCKPG
                                                                                                         84 GPCTGHLSE-S-QPCDRTHDRVCNCSTG 109
                                                                                                                                              35 CAG-DFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQ 93
                                                                                                                                                                                 28 CGGHDYEKD-GL-CCASCHPGFYASRLCG-PGSNTVCSPCEDGTFTA-STNHAPACVSCR 83
                                                                                                                                                                                                                                      5.18;
Similarity 33.08;
                                                                                                                                                                                                                                                                                                 #length 325
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                           homology
                                                                                                                                                                                                                                                                                             #domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3
$\frac{1}{2}$ #molecular-weight 35132 #checksum 4629
               25
             22:24:41 2000
                                                                                                                                                                                                                       Score 164; DB 2;
Pred. No. 7.46e-10;
15; Mismatches 36
                                                                      120
                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                          Length 325;
                                                                                                                                                                                                                       Gaps
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:24:59 2000; MasPar time 13.86 Seconds 712.501 Million cell updates/sec

Tabular output not generated.

Title: >US-09-314-889-4 (1-417) from US09314889.pep 3198

Sequence: Description: Perfect Score: 1 MEQRPRGCAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP 417

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq36 1:geneseqp

Statistics: Mean 35.628; Variance 153.996; scale 0.231

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

- Re	Result No.	Score	Query Match I	Length I	DB	ID	Description	Pred. No.
	_	3198	100.0	417	⊢	W31517	Death domain containin	6.61e-300
,	2	3198	100.0	417	۳	W95538	domain	6.61e-300
	w	3198	100.0	417	_	W57045	Human apoptosis induci	6.61e-300
	4	3198	100.0	417	Ц	W26709	Human apoptosis protei	6.61e-300
	ر.	3198	100.0	833	٢	W64486		6.61e-300
	6	3118	97.5	428	۲	W31516	doma	6.01e-292
1	7	3118	97.5	428		W95537	Death domain containin	6.01e-292
•	æ	1962	61.4	411	ب	W57046	Mouse apoptosis induci	2.99e-177
	9	1422	44.5	181	μ	W26708	Human apoptosis protei	
	10	503	15.7	65	۳	W93610	Human DR3 protein frag	6.46e-35
	11	412	12.9	909	۲	W64485	Human Fas protein.	2.15e-26
	12	408	12.8	455	۳	R07451	Human Tumour Necrosis	.05e-
	13	407	12.7	455	۲	R10986	30kD TNF inhibitor pre	6.26e-26
	14	407		455	سر	R75084	p55 TNF-R.	6.26e-26
	<u>1</u> 2	407	12.7	455	1	R42059	Lambda derived TNF-R.	6.26e-26
	16	404		455	1	R11082	Human 55kD TNF-binding	1.19e-25
	17	404	12.6	455	_	R20787	TNF-alpha binding prot	.19e-
	18	400		443	1	R51033	tumour	2.79e-25
	19	400	12.5	455	1	R51034	Mutant p55 tumour necr	.79e-
	20	400		455	_	R42197	p55 Tumour necrosis fa	2.79e-25
	21	394	12.3	455	1	R12550	Type I TNF receptor.	1.00e-24
	22	387	12.1	433	_	R51032	Mutant p55 tumour necr	4.46e-24
	23	372	11.6	455	_	R24000	TNF-alpha 55kD recepto	1.08e-22

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24
240	243	246	246	246	246	246	246	246	246	246	246	246	246	247	246	246	245	250	248	273	100
7.5	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8	8.5	TI.U
161	884	1604	1245	900	547	451	420	417	397	371	366	311	309	285	211	199	108	336	307	256	401
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R27496	R70109	R70105	R70106	R70103	R70104	R70107	W89224	W89226	W89227	R07449	W89228	W89229	R70108	W33359	W89225	R24080	W73570	W33360	W33358	W33357	X0/450
Native 30 kD TNF inhib	TNF-R-GBP 130 fusion p	TNF-R-EBA 175 fusion p	TNF-R-Pl. vivax Duffy	TNF-R-GBP 130 fusion p	TNF-R-GBPH fusion prot	TNF-R-GBP 130 fusion p	Tumour necrosis factor	TNF-R-GBPH fusion prot	TBP(20-190)/hCG-alpha	Tumour necrosis factor	Truncated TNF-alpha 55	Cytoplasmic domain of	TBP(20-190)/hCG-beta f	TBP(20-161)/hCG-beta f	TBP(20-161)/hCG-alpha	Rat Tullour Necrosis ra					
8.70e-1	4.75e-1	2.59e-11	2.59e-11	2.59e-11	2.59e-11	2.59e-11	2.59e-11	2.59e-11	2.59e-11	2.59e-1	2.59e-11	2.59e-11	2.59e-1	2.11e-11	2.59e-11	2.59e-11	3.17e-11	1.15e-11	1.73e-11	1.05e-13	9.19e-21

## ALIGNMENTS

នៃនិនិនិនិនិ	888	ននន	PS PS	T T T	DR DR	PI	PR PA	PF	PN	T 1	FT.	7 'F	FT	FT	H 1	9 E	SO	X X	DE	DT A	RESULT
DR3 can be expressed in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the inhibition of apoptosis, or to screen for modulator compounds. Antagonists, such as antibodies raised against DR3-V1, can be used to treat diseases and disorders associated with increased apoptosis and for treating inflammatory diseases and disorders. Sequence 417 AA;	domain containing receptor DR3-V1 (see W31516) has also been identified. Recombinant full-length or mature DR3, or the overracellular transmembrages intracellular or death domain of	DR3, a novel member of the tumour necrosis factor receptor family. Its amino acid sequence was deduced from a cDNA clone (see T89427) isolated from a HUYEC cDNA library. Related death	to treat initalmmatory diseases Claim 1; Page 75-77; 108pp; English. This protein comprises human death domain containing receptor	Death domain containing receptor polypeptide(s) DR3 and DR3-V1 for activation of apoptosis and NF-kappaB, antagonists can be used		(UNMI) UNIV MICHIGAN. Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;	12-mar-1996; US-013285. (HUMA-) HUMAN GENOME SCI INC.	18-SEP-1997. 17-OCT-1996; U16849.		Domain 342408 /note= "death domain"		/note= "transmembrane domain"	Domain 202224		/label= Siq_peptide	100	o sapiens.		n containing	W3151/; 02-MAR-1998 (first entry)	LT 1 W31517 standard; Protein; 417 AA.

Query Match Best Local

Score 3198; DB 1; Pred. No. 6.61e-300;

Length 417;

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                                                                                          Matches
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12-MAR-1997; 057503.
06-FEB-1997; US-037341.
12-MAR-1996; US-013285.
17-OCT-1996; US-028711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMAN GENOME SCI INC
(UNMI) UNIV MICHIGAN.
WPI; 99-124390/71
                                                                                                                                                                                                                                                                                                                                                                                                                           New death domain containing receptor and recombinant vector optionally comprising leader sequence Claim 1; Fig 3; 50pp; Japanese.

The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DN3-V1 and DR3. The DR3-V1 CDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757, Recombinant vectors comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W95538 standard;
W95538;
                                                                                                                                                                                                                                                                                                     the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents the amino acid sequence of a death domain containing receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Death domain containing receptor polypeptide (DR3). Death domain; receptor; DR3-V1; DR3; recombinant.
                                                                                                                                                                                                                                   Sequence
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                                                                  Local Similarity 100.

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           1 MEQRPRGCAAVAAALLLIVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                      e 3198; DB 1;
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Mismatches 0;
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Best Local
                                                                                                                                                                                                                                      DNA encoding apoptosis inducing receptor - which is Type I transmembrane protein, useful for regulating cell death claim 16; Page 28-30; 45pp; English.

This sequence is the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can also be used in vitro to block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or T cells expressing AIR in autoimmune diseases. Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human apoptosis inducing receptor.

Apoptosis inducing receptor; AIR protein; human; Apoptosis inducing receptor; tumour cell death;
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04-OCT-1996; US-044456.
(IMMV ) IMMUNEX CORP.
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molecules comprising Apo-3 fused to a heterologous amino acid
c sequence; antibodies that bind to Apo-3 or its extracellular
domain; nucleic acids encoding the polypeptides, as well as
vectors and host cells; a non-human transgenic animal containing
c cells that express nucleic acid encoding Apo-3; and a non-human
knockout animal containing cells having an altered Apo-3 gene.
Apo-3 can be used to induce apoptosis or NF-kappa-B- (Nf-kB)- or
JNK-mediated gene expression for therapeutic purposes. Apo-3-IgG
fusion proteins can be used to inhibit apoptosis or NF-kB
induction or JNK activation for therapeutic purposes, and can
be used as immunogens for anti-Apo-3- antibody production.
Apo-3 or Apo-2LI can also be used as assay standards. The
animals can be used in drug screening and development.
                                                                                                                                                                                          in mammalian cells
Claim 19; Page 46-48; 70pp; English.
Claim 19; Page 46-48; 70pp; English.
This novel polypeptide, designated Apo-3, is a protein that stimulates or induces apoptotic activity in mammalian cells purposes. Its amino acid sequence was deduced from a human foetal heart cDNA clone (see T9180). The N-terminal 181 amino acids of Apo-3 are identical to the sequence of another novel apoptosis polypeptide, Apo-2LI (see W26709). Also claimed are: polypeptides comprising the extracellular or death domain of Apo-3; chimeric
                                                                                                                                                                                                                                                                                                                               Polypeptide(s) Apo-3 and Apo-2LI -
                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T91180
                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1996; US-710802.
01-APR-1996; US-625328.
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              PS Disclosure; Fig 2; 92pp; English.

C This sequence represents the human death domain containing receptor-3

C DR3 which is used in a method resulting in the isolation of a human death domain containing receptor 4, DR4. DR4 agonists are used to increase apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of cancer, autoimmune disease, viral or other infections, and inflammation, graft vs. host disease, acute or chronic graft rejection. Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune deficiency syndrome, neurodegenerative disease, acquired immune deficiency syndrome, neurodegenerative disease, cacquired immune deficiency syndrome, neurodegenerative disease, septic shock, cachexia and anorexia, also a wide range of inflammatory conditions. DR4 of fragments of the protein are used diagnostically, e.g. to detect mutant forms of DR4 (possibly associated with disease), for conditions of the DR4 gene or related sequences and for chromosomal mapping.
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(UNMI ) UNIV MICHIGAN
Dixit VM, Gentz RL, N
WPI; 98-427952/36.
                                                                                                                                                                                                                                                                                                                                                                                                          useful for therapeutic modulation of apoptosis, in e.g. cancer autolimnune diseases
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W31516
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02-MAR-1998
        18-SEP-1997.
17-OCT-1996; U16849.
12-MAR-1996; US-013285.
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J11000170-A.

06-CAN-1999.

12-MAR-1997; 057503.

16-FEB-1997; US-037341.

2 12-MAR-1996; US-013285.

R 17-OCT-1996; US-028711.

R 17-OCT-1996; US-028711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 71-73; 108pp; I
This protein comprises human
DR3-V1, a note member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T89426.
Death domain containing recefor activation of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ, Dixit WPI; 97-470812/43.
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                                                                                                                                                                                                                                                                                                            Death domain;
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                                                                                                                                                                                                                                                                                      Homo
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25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                     W95537 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V1, a novel member of the tumour necrosis factor
ly. Its amino acid sequence was deduced from a c
T89426) isolated from a human testis tumour libr
                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCXPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 134
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                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 428
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                                                                                                                                                                                                                                                                                                            receptor polypeptide (DR3-V1).
DR3-V1; DR3; recombinant.
                     INC
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e 3118; DB 1;
. No. 6.01e-292;
Mismatches 4;
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Best Loc
Matches
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The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents the amino acid sequence of a death domain containing receptor polypeptide (DR3-V1).
DNA encoding apoptosis inducing receptor - which is Type I transmembrane protein, useful for regulating cell death claim 16; Page 33-35; 45pp; English.

This sequence is the mouse apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of w can be used to regulate cell death in a therapeutic setting. Soluble can also be used in vitro to block apoptosis or AIR-expressing cells
                                                                                                   Perkins
WPI; 98-
                                                                                                                         09-APR-1998.
03-OCT-1997; U17876.
04-OCT-1996; US-044456.
(IMMY) IMMUNEX CORP.
                                                                                                                                                                                                          Mouse apoptosis inducing receptor.
Apoptosis inducing receptor; AIR protein;
Type I transmembrane protein; tumour cell
                                                                                        N-PSDB; V28701.
                                                                                                                                                                           WO9814565-A1.
                                                                                                                                                                                                  therapy.
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                                                                                                   98-240077/21.
                                                                                                                                                                                                                                                                                                                       PSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEA
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99-124390/11.
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larity 98.3%;
Conservative
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                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                         411
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Pred. No. 6.
3; Mismatc
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.01e-292;
                                                                                                                                                                                                             mouse;
death;
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                                                                                                                                                                                                             cell death autoimmune
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  Soluble AIR or cells, or
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Best Loc
Matches
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31-MAR-1997; 1
23-SEP-1996; 1
01-APR-1996; 1
Claim 1; Page 43-44; 70pp; English.

This novel polypeptidede, designated Apo-2 ligand inhib (Apo-2LI), can be used to inhibit apoptosis for therape purposes. Its amino acid sequence was deduced from a h cDNA clone (see T91179) and is identical to amino acid 1-181 of another novel apoptosis polypeptide, Apō-3 (se W25709). It may be a soluble, truncated of secreted fo lacking some extracellular sequence as well as the tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human apoptosis protein Anapor-2LI; apontor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to screen agonists or antagonists of AIR activity. The cytoplasmic of AIR can be used to develop assays for inhibitors of AIR-induced death, which is useful to regulate cell death in a therapeutic sett well as in vitro. Agonists of AIR activity can be used to kill tume cells that express AIR, or T cells expressing AIR in autoimmune dis
                                                                                                                                                               in mammalian cells
Claim 1; Page 43-44;
                                                                                                                                                                                                                                                           (GETH ) GENENTECH
Ashkenazi AJ;
WPI; 97-503105/46.
                                                                                                                                                                                                             Polypeptide(s) Apo-3 and Apo-2LI - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W26708
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|DQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
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411 AA;
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US-710802.
US-625328.
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67
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106
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d. No. 2.99e-177;
Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor;
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    secreted form of as the transmemb:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
                                                                                                                      for therapeutic
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Matches 6
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Best Local S
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10-JUL-1998; U14495.

11-MAR-1998; US-077661.

11-JUL-1997; US-052305.

04-AUG-1997; US-064710.

30-SEP-1997; US-060473.

11-MAR-1998; US-077526.

11-MAR-1998; US-077628.
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                                                                                                                                                                                                                                                                                            extracellular receptor, transmembrane and death domains. The nucleic acid molecule which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful in the diagnosis and treatment of neoplastic diseases. The invention is also useful for the production of animal model systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human adriamycin-inducible killer protein located on chromosome 8p21, which also has p53-inducible, apoptosis-mediating activity and comprises an amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               induces apoptosis and is useful in neoplastic diseases
Disclosure; Page 46; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DR3 protein; addriamycin inducible; human;
Killer protein; addriamycin inducible; human;
p53-inducible; apoptosis-mediating activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            El-Deiry WS;
WPI; 99-120857/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W93610 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quantitative diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9902653-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplastic disease;
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                                                        346
  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       new nucleic acid encodes a p53
nduces apoptosis and is useful
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                                                        RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC 405
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                                                                                                                                                                h 15.7%;
Similarity 100.0%;
65; Conservative
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Similarity 100.0%;
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Pred. No. 5.28e-124;
                                                                                                                                                             Pred. No. 6.46e
0; Mismatches
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No. 6.46e-35;
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diagnosis
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and treat
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animal model;
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Disclosure; Fig 2; 92pp; English.

This sequence represents the human fas protein which is used in a method resulting in the isolation of a human death domain containing receptor 4, presulting in the isolation of a human death domain containing receptor 4.

DR4. DR4 agonists are used to increase apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in cases of cancer, autoimmune disease, viral or other infections, inflammation, graft vs. host disease, acute or chronic graft rejection. Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of acquired immune deficiency syndrome, neurodegenerative disease, myelodysplastic syndrome, ischaemic injury, toxin-induced liver damage, septic shock, cachexia and anorexia, also a wide range of inflammatory conditions. DR4 of fragments of the protein are used diagnostically, e.g. to detect mutant forms of DR4 (possibly associated with disease), for isolating the DR4 gene or related sequences and for other and acceptances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens. W09832856-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding human death useful for therapeutic modulation autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(UNMI) UNIV MICHIGAN.
Dixit VM, Gentz RL, Ni J, Pan
WPI; 98-427952/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1998.
27-JAN-1998; U01464.
25-FEB-1997; US-037829.
05-FEB-1997; US-035722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Fas protein.
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20-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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   TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP--
                                                                                                                                                                                                                                                                   A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                             GELEGITTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ 75
                                                                   RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                                                                              PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLKWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
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128; Conse
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llarity 30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 412; DB 1;
Pred. No. 2.15e-26;
81; Mismatches 175
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AGLGAVYAALERMGLDGCVED
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Schoolscure; Fig 91(1-2), 51pp; German.

CraTNF-R8 (Q06284) was used to screen the HS913T cDNA library.

ClambdaTNF-R2 encodes the complete human TNF-R2 and was used to construct a plasmid (pADTNF-R) expressing the product the same way as pADTNF-BP (see Q06282). The expressing the product the same way as pADTNF-BP (see Q06282). The expressing the product the same way as pADTNF-BP (see Q06282). The expressing the product the same way as pADTNF-BP (see Q06282). The expressing the product the same way as padTNF-BP (see Q06282). The expressing the product the damaging effects of TNF-alpha or -beta (e.g. infectious or parasitic diseases, shock, cachexia, autoimmune diseases, adult respiratory distress syndrome etc., or side effects of treatment with CTNG-alpha). They can also be used as diagnostic reagents for assaying TNF and in study of TNF-receptor interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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21-APR-1989; DE-913101.
21-JUN-1989; DE-920282.
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29-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                       GELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
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                                                                                                         RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                                                                                                                                                                                                                                                         A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIQNVKGTEDSGTTVLLP-LVIFFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC-
IEEAL
                                                         TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
                                                                                                                                                                                                   -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                                                                                                                                                                                                                                                    PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
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Pred. No. 5.05e-26;
81; Mismatches 177;
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Best Local
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library prepd. from RNA torm U93/ cetts treated with the whole gene can be inserted into expression vectors for prepn of TNF inhibitor for use in the treatment of inflammatory and the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUL-1990;
18-JUL-1989;
11-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and -beta, useful as therapeutic agent.
Disclosure; Fig 21; 142pp; English.
The sequence comprises the entire 30 kD TNF inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 91-073847,
N-PSDB; Q10883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor inhibitor - for suppression
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24-JAN-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from which the sequence was deduced was isolated from a cDNA library prepd. from RNA form U937 cells treated with PMA/PHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYNE-) SYNERGEN INC. WPI; 91-073847/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30kD TNF inhibitor
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     LRSRL
                                                  IEEAL
                                                                                               TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVED
                                                                                                                                          RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED
                                                                                                                                                                                                                                            PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR
                                                                                                                                                                                                                                                                                         A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                                                                                      AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYCQPCLDCGALHRHTRLLC - SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG - SCPERC - A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC-
                                                                                                                                                                                            -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
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127; Conse
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; US-450329.
; US-479661.
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larity 29.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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ctor; inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The active protein is claimed (Claim
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81; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 407;
Pred. No. 6.
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5.26e-26;
ches 177;
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RESULT

R75084 standard; Protein; 455 R75084; 19-JAN-1996 (first entry)

p55 TNF-R

TNF-R; human; murine; chimera;

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CC This sequence represents human p55 tumour necrosis factor (TNF-R). CC This sequence represents human p55 tumour necrosis factor (TNF-R). CC Expression of this receptor is regulated by shedding of the extracellular CC contents, e.g. phorbol myristate acetate (PMA), depending on cell cinducing agents, e.g. phorbol myristate acetate (PMA), depending on cell cype. The only region of the receptor whose structure affects the CC shedding response is the spacer region (see R75012) in the extracellular CC domain. This region is located close to a site of cleavage of the CC molecule, and links the Cys rich module to the transmembrane domain. The CC spacer region of the encoded protein was used to create the chimeras between human p55 TNF-R and murine epidermal growth factor receptor CC (EGF-R) that are represented by R75007-11. This spacer region was CC subjected to deletion mutations (R75013-25) and substitutions CC (R75026-47). Of the spacer region, the most important residues are CC (R75026-47). Lys 174 and Gly 175, with Val 173 being the most conformation of these residues, with the exception of a limited CC dependence on the identity of Val 173. Mutations which alter the CC conformation of the protein adversely effect the shedding process. The mutations shown in R75013-47 were introduced in order to create an CC inhibitor of a protease that is capable of cleaving the soluble TNF-R CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in CC sequence of Fragments of These protease inhibitors can be used for enhancing TNF function.
                                                                                                            Query Match
Best Local
                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protease capable of cleaving soluble tumour necrosis (TNF) receptor - from cell-bound TNF- receptor, useful f antagonising deleterious effects of TNF.
Disclosure; Fig 1; 40pp; English.
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N-PSDB; Q90513.
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Batkin M, Brakebusch C,
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11-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU9475742-A.
                                                                                                                                                                               Sequence
19
                                           27
                                                                                                            Local Similarity
                                           VIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECES
LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
                                                                                                                                                                                 455 AA;
                                                                                        Conservative
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203
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201
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212. .234
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193. 210
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145. .
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54. .5
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e acetate;
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29.9%;
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Varfolomeev
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81; M
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No. 6.
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5.26e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor; IL-IR; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria; rheumatoid arthritis; diabetes; multiple sclerosis; septic shock; pulmonary fibrosis; silicosis; allograft; xenograft; rejection; graft verses host disease; sepsis; inflammation; allergy;
                                                                                                                                                       New fusion protein tumour necrosis factor and human interleukin-1 receptor - useful in therapy, diagnosis and assays of e.g. rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc. Disclosure; Page 57-59; 85pp; English.

The sequences given in R42058-59 repressent human tumour necrosis factor receptor (TNF-R) and the sequences in R42060-61 represent human interleukin-1 receptor (IL-IR). These sequences were used the production of a fusion protein which conformed to one of the
The linker may comprise 5-100 amino acids selected from Gly, Asp, Ser, Thr and Ala. These linkers separate the individual moetities by such a distance that each component of the fusion protten is capable of folding into the secondary or tertiary structure requirements of the secondary or tertiary structure requirements biological activity. These fusion proteins may be used in
                                                                                                                                                                                                                                                                                                                                                                       WO9319777-A.
14-OCT-1993.
26-MAR-1993; UO2938.
30-MAR-1992; US-860710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1994 (first entry) Lambda derived TNF-R.
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29-APR-1994
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R42059 standard; Protein; 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune dysfunction
                                                                                                      TNF-R-linker-TNF-R-linker-TL-1R
IL-1R-linker-TNF-R
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                                                                                       TNF-R-linker-TNF-R
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                                                                                                                                                                                                                                                                                                                                      Smith CA;
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41. .455
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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                     structure required
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Query Match
Best Local 9
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409 LRSRL 413
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                                                                                                                                                                                                                                                 317 PYQGADPILATALASDPIPNPLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVR 376
                                                                                                                                                                                                                                                                                                                 243 A-LTPPPATHLSPLDS-AHTL-LAPPDSSEKICTVQLVGNS-WTPGYPETQEALCPQVT-
                                                                                                                                                                                                                                                                                                                                                   257 GELEGTTTKPLAPNPSFSPTPGFTPTLGFSPVPSSTFTSSSTYTPGDCPNFAAPRREVAP 316 : | : | : | | | | | : |:
                                                                                                                                                                                                                                                                                                                                                                                                                         193 AVCGWROMF-W-VQVLLAGLVV--PL-LLGATLT-YTYR-HCWPHK--PLVTADEA-GME 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 FNCSLCLN-GTVH----LSCQEKQNTVC-TCHAGFFLRENECVSCSNCKKSLECTKLCLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 DTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 LLGARAQGGTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity tes 127; Conser
                                                                                                                                                 RLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLED 436
                                                                                                       TLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIENVKGTEDSGTTVLLP-LVIFFGLCLLSLLFIGLMYRYQRWKSKLYSIVCGKSTPEKE 256
                                                                                                                                                                                                            -W-SWDQLPSRALGPAAAPT-LSP-ESPAGSPAMMLQPGPQ-LYDVMDAVPARRWKEFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIGLVPHLGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECES 86
                                                     IEEAL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPTSTLG-SCPERC-A 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYW-SENLFQC- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
llarity 29.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 407; DB 1; Le
Pred. No. 6.26e-26;
81; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                       408
                                                                                                                                                                                                               352
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